

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 24, 2002, 10:09:06 ; Search time 13.1116 Seconds  
(without alignments)  
527.349 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242

Sequence: 1 MTIVAPAMSPPTTYLLLLLL.....RPGQVPVPSPDQLLVEH 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*

2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*

3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*

4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*

5: /cgn2\_6/ptodata/1/1aa/PCrus.COMB.pep.\*

6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	1	US-08-243-545-6
2	1242	100.0	235	2	US-08-993-962-6
3	1242	100.0	235	4	US-09-160-841-6
4	1242	100.0	235	4	US-09-109-100-1
5	1242	100.0	235	5	PCR-US94-05365-6
6	1124	90.5	212	4	US-09-109-100-10
7	1114	89.7	209	4	US-09-109-100-18
8	1110	89.4	209	4	US-09-109-100-9
9	1110	89.4	209	4	US-09-109-100-12
10	1110	89.4	209	4	US-09-109-100-14
11	1110	89.4	209	4	US-09-109-100-17
12	1108	89.2	209	4	US-09-109-100-11
13	1108	89.2	209	4	US-09-109-100-15
14	1107	89.1	209	4	US-09-109-100-13
15	1106	89.0	209	4	US-09-109-100-8
16	1100	88.6	209	4	US-09-109-100-16
17	768.5	61.9	231	1	US-08-243-545-2
18	768.5	61.9	231	2	US-08-993-962-2
19	768.5	61.9	231	4	US-09-160-841-2
20	768.5	61.9	231	5	PCR-US94-05365-2
21	765.5	61.6	231	1	US-08-220-378B-7
22	765.5	61.6	231	1	PCR-US95-03866-6
23	506.5	40.8	137	4	US-09-109-100-19
24	154	12.4	42	5	PCR-US94-05150-17
25	91.5	7.4	675	1	US-08-317-522A-9
26	91.5	7.4	675	1	US-08-439-818A-9
27	91.5	7.4	675	2	US-08-751-965-9

28	91.5	7.4	675	2	US-08-738-975-9	Sequence 9, Appli
29	91.5	7.4	675	2	US-08-728-626-9	Sequence 9, Appli
30	91.5	7.4	675	3	US-08-808-599A-9	Sequence 9, Appli
31	87.5	7.0	415	4	US-09-006-353A-6	Sequence 6, Appli
32	87.5	7.0	415	4	US-09-573-986-6	Sequence 6, Appli
33	85	6.8	366	1	US-08-004-492-8	Sequence 8, Appli
34	84.5	6.8	913	1	US-08-445-640-4	Sequence 4, Appli
35	84.5	6.8	913	3	US-08-170-558-4	Sequence 4, Appli
36	84.5	6.8	913	3	US-08-447-314-4	Sequence 4, Appli
37	84.5	6.8	913	3	US-08-445-461-4	Sequence 4, Appli
38	84	6.8	107	4	US-09-220-528-52	Sequence 52, Appli
39	84	6.8	220	4	US-09-220-528-26	Sequence 26, Appli
40	83.5	6.7	429	1	US-07-964-589-2	Sequence 2, Appli
41	83.5	6.7	429	5	PCR-US93-02024-2	Sequence 2, Appli
42	83.5	6.7	671	3	US-09-121-321-16	Sequence 16, Appli
43	83.5	6.7	671	4	US-08-933-803A-16	Sequence 16, Appli
44	83	6.7	28	5	PCR-US94-05150-12	Sequence 12, Appli
45	83	6.7	758	1	US-07-756-250-16	Sequence 16, Appli

## ALIGNMENTS

RESULT 1  
US-08-243-545-6  
; Sequence 6, Application US/08243545  
; Patent No. 5554512  
; GENERAL INFORMATION:  
; APPLICANT: Lyman, Stewart D.  
; TITLE OF INVENTION: Ligands for flt3/Flk-2 Receptors  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: Apple Macintosh  
; SOFTWARE: Microsoft Word, Version #5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/243,545  
; FILING DATE: 11-MAY-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/162,407  
; FILING DATE: 03-DEC-1993  
; APPLICATION NUMBER: 08/111,758  
; FILING DATE: August 25, 1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/106,463  
; FILING DATE: August 12, 1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Malaska, Stephen L.  
; REGISTRATION NUMBER: 32,655  
; REFERENCE/DOCKET NUMBER: 2813-C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELE: 756822  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 235 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-243-545-6

Query Match 100.0%; Score 1242; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1.7e-117;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGSLSGTQDCSFQHSPISSDPAVKIRLSYLLQDYPTV 60  
Db 1 MTVLAPAMSPPTTYLLLLSSGSLSGTQDCSFQHSPISSDPAVKIRLSYLLQDYPTV 60  
QY 61 ASNLODEELCGIMRLVLAQRMMERLKTAVAGSKMOGLLEERVNTEIHFTVKCAFPSPSCL 120  
Db 61 ASNLODEELCGIMRLVLAQRMMERLKTAVAGSKMOGLLEERVNTEIHFTVKCAFPSPSCL 120  
QY 121 RFOVTNISRLLOETSEQLVALKPWITTRONFSRCLQLCCPDSSSTLPPMSPRPLEATAPT 180  
Db 121 RFOVTNISRLLOETSEQLVALKPWITTRONFSRCLQLCCPDSSSTLPPMSPRPLEATAPT 180  
QY 181 APOPLLILLLLPYGLLLAAACLIHMQRTRRRTPRGEQVPPVPSFODLLVEH 235  
Db 181 APOPLLILLLLPYGLLLAAACLIHMQRTRRRTPRGEQVPPVPSFODLLVEH 235

#### RESULT 2

US-08-993-962-6  
Sequence 6, Application US/08993962

Patent No. 5843423

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.

APPLICANT: Beckmann, M. Patricia

TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Stephen L. Malaska, Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.0.1

SOFTWARE: Microsoft Word, Version #5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/993,962

FILING DATE: December 18, 1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/162,407

FILING DATE: December 3, 1993

APPLICATION NUMBER: 08/111,758

FILING DATE: August 25, 1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/106,463

FILING DATE: August 12, 1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/068,394

FILING DATE: May 24, 1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655

REFERENCE/DOCKET NUMBER: 2813-C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-993-962-6

Query Match 100.0%; Score 1242; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1.7e-117;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGSLSGTQDCSFQHSPISSDPAVKIRLSYLLQDYPTV 60  
Db 1 MTVLAPAMSPPTTYLLLLSSGSLSGTQDCSFQHSPISSDPAVKIRLSYLLQDYPTV 60  
QY 61 ASNLODEELCGIMRLVLAQRMMERLKTAVAGSKMOGLLEERVNTEIHFTVKCAFPSPSCL 120  
Db 61 ASNLODEELCGIMRLVLAQRMMERLKTAVAGSKMOGLLEERVNTEIHFTVKCAFPSPSCL 120  
QY 121 RFOVTNISRLLOETSEQLVALKPWITTRONFSRCLQLCCPDSSSTLPPMSPRPLEATAPT 180  
Db 121 RFOVTNISRLLOETSEQLVALKPWITTRONFSRCLQLCCPDSSSTLPPMSPRPLEATAPT 180  
QY 181 APOPLLILLLLPYGLLLAAACLIHMQRTRRRTPRGEQVPPVPSFODLLVEH 235  
Db 181 APOPLLILLLLPYGLLLAAACLIHMQRTRRRTPRGEQVPPVPSFODLLVEH 235

#### RESULT 3

US-09-160-841-6  
Sequence 6, Application US/09160841

Patent No. 6190655

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.

APPLICANT: Beckmann, M. Patricia

TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Stephen L. Malaska, Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.0.1

SOFTWARE: Microsoft Word, Version #5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/160,841

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/162,407

FILING DATE: December 3, 1993

APPLICATION NUMBER: 08/111,758

FILING DATE: August 25, 1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/106,463

FILING DATE: August 12, 1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/068,394

FILING DATE: May 24, 1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655

REFERENCE/DOCKET NUMBER: 2813-C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

TELEX: 756822

```
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 235 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-160-841-6

Query Match      100.0%; Score 1242; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDFAVKIRLSYLLQDYPVTV 60
    |||||||
DB 1 MTVLAPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDFAVKIRLSYLLQDYPVTV 60

QY 61 ASNLODEELCGIMRLVLAQRMERLKTIVAGSKMOGLLEEVNTEIHFTVCARQPPSCL 120
    |||||||
DB 61 ASNLODEELCGIMRLVLAQRMERLKTIVAGSKMOGLLEEVNTEIHFTVCARQPPSCL 120

QY 121 REVQTNISRLQETSEOLVALKPMWTRONFSRCLELOCQPDSSTLPPWSPRPLEATAPT 180
    |||||||
DB 121 REVQTNISRLQETSEOLVALKPMWTRONFSRCLELOCQPDSSTLPPWSPRPLEATAPT 180

QY 181 APQPLLLLLLPVGLLLAAAMCLHMQRTRRTPRPEGVPPVPSQDILLVEH 235
    |||||||
DB 181 APQPLLLLLLPVGLLLAAAMCLHMQRTRRTPRPEGVPPVPSQDILLVEH 235

RESULT 4
US-09-109-100-1
; Sequence 1, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-109-100-1

Query Match      100.0%; Score 1242; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDFAVKIRLSYLLQDYPVTV 60
    |||||||
DB 1 MTVLAPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDFAVKIRLSYLLQDYPVTV 60

QY 61 ASNLODEELCGIMRLVLAQRMERLKTIVAGSKMOGLLEEVNTEIHFTVCARQPPSCL 120
    |||||||
DB 61 ASNLODEELCGIMRLVLAQRMERLKTIVAGSKMOGLLEEVNTEIHFTVCARQPPSCL 120

QY 121 REVQTNISRLQETSEOLVALKPMWTRONFSRCLELOCQPDSSTLPPWSPRPLEATAPT 180
    |||||||
DB 121 REVQTNISRLQETSEOLVALKPMWTRONFSRCLELOCQPDSSTLPPWSPRPLEATAPT 180

QY 181 APQPLLLLLLPVGLLLAAAMCLHMQRTRRTPRPEGVPPVPSQDILLVEH 235
    |||||||
DB 181 APQPLLLLLLPVGLLLAAAMCLHMQRTRRTPRPEGVPPVPSQDILLVEH 235

RESULT 5
PCT-US94-05365-6
; Sequence 6, Application PC/TUS9405365
; GENERAL INFORMATION:
```

```
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05365
; FILING DATE: May 24, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: -to be assigned-
; FILING DATE: May 11, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,502
; FILING DATE: March 7, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/162,407
; FILING DATE: December 3, 1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 235 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-05365-6

Query Match      100.0%; Score 1242; DB 5; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDFAVKIRLSYLLQDYPVTV 60
    |||||||
DB 1 MTVLAPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDFAVKIRLSYLLQDYPVTV 60

QY 61 ASNLODEELCGIMRLVLAQRMERLKTIVAGSKMOGLLEEVNTEIHFTVCARQPPSCL 120
    |||||||
DB 61 ASNLODEELCGIMRLVLAQRMERLKTIVAGSKMOGLLEEVNTEIHFTVCARQPPSCL 120

QY 121 REVQTNISRLQETSEOLVALKPMWTRONFSRCLELOCQPDSSTLPPWSPRPLEATAPT 180
    |||||||
```

```
Db 121 RFVQINISRLQETSEQVIAKPMITRQNSRCLQCOQPPSSSTLPPWSPRLPEATPT 180
QY 181 APQPLLLLLLPGVGLLLAAACMLHWQTRRRTPRGEQVPPVPSQDILLVEH 235
Db 181 APQPLLLLLLPGVGLLLAAACMLHWQTRRRTPRGEQVPPVPSQDILLVEH 235
```

RESULT 6  
US-09-109-100-10  
; Sequence 10, Application US/09109100C  
; Patent No. 6291661  
; GENERAL INFORMATION:

```
; APPLICANT: McGraw, Thomas J.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-10
```

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.2e-105;  
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 25 SGTQCSFQHSPISSDFAVKIRELSDYLLQDYPVTASNLODEELCGGLMRLVLAQRME 84
Db 2 SGTQCSFQHSPISSDFAVKIRELSDYLLQDYPVTASNLODEELCGGLMRLVLAQRME 61
```

```
QY 85 RLKTVAGSKMOGLERVNTIEHFVTKCAFQPPSCLRFVQTNISRLQETSEQVIAKPM 144
Db 62 RLKTVAGSKMOGLERVNTIEHFVTKCAFQPPSCLRFVQTNISRLQETSEQVIAKPM 121
```

```
QY 145 ITRQNSRCLQCOQPPSSSTLPPWSPRLPEATPTAQPPLLLLLLPGVGLLLAAAC 204
Db 122 ITRQNSRCLQCOQPPSSSTLPPWSPRLPEATPTAQPPLLLLLLPGVGLLLAAAC 181
```

```
QY 205 LHMQTRRRTPRGEQVPPVPSQDILLVEH 235
Db 182 LHMQTRRRTPRGEQVPPVPSQDILLVEH 212
```

RESULT 7  
US-09-109-100-18  
; Sequence 18, Application US/09109100C  
; Patent No. 6291661  
; GENERAL INFORMATION:

```
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGraw, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-18
```

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.2e-104;  
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 27 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTASNLODEELCGGLMRLVLAQRME 86
Db 27 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTASNLODEELCGGLMRLVLAQRME 86
```

```
Db 1 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTASNLODEELCGGLMRLVLAQRME 60
QY 87 KTVAGSKMOGLERVNTIEHFVTKCAFQPPSCLRFVQTNISRLQETSEQVIAKPMIT 146
Db 61 KTVAGSKMOGLERVNTIEHFVTKCAFQPPSCLRFVQTNISRLQETSEQVIAKPMIT 120
```

```
QY 147 RQNSRCLQCOQPPSSSTLPPWSPRLPEATPTAQPPLLLLLLPGVGLLLAAAC 206
Db 121 RQNSRCLQCOQPPSSSTLPPWSPRLPEATPTAQPPLLLLLLPGVGLLLAAAC 180
```

```
QY 207 WQTRRRTPRGEQVPPVPSQDILLVEH 235
Db 181 WQTRRRTPRGEQVPPVPSQDILLVEH 209
```

RESULT 8  
US-09-109-100-9  
; Sequence 9, Application US/09109100C  
; Patent No. 6291661  
; GENERAL INFORMATION:

```
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGraw, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-9
```

Query Match  
Best Local Similarity 99.5%; Pred. No. 3e-104;  
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 27 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTASNLODEELCGGLMRLVLAQRME 86
Db 1 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTASNLODEELCGGLMRLVLAQRME 60
```

```
QY 87 KTVAGSKMOGLERVNTIEHFVTKCAFQPPSCLRFVQTNISRLQETSEQVIAKPMIT 146
Db 61 KTVAGSKMOGLERVNTIEHFVTKCAFQPPSCLRFVQTNISRLQETSEQVIAKPMIT 120
```

```
QY 147 RQNSRCLQCOQPPSSSTLPPWSPRLPEATPTAQPPLLLLLLPGVGLLLAAAC 206
Db 121 RQNSRCLQCOQPPSSSTLPPWSPRLPEATPTAQPPLLLLLLPGVGLLLAAAC 180
```

```
QY 207 WQTRRRTPRGEQVPPVPSQDILLVEH 235
Db 181 WQTRRRTPRGEQVPPVPSQDILLVEH 209
```

RESULT 9  
US-09-109-100-12  
; Sequence 12, Application US/09109100C  
; Patent No. 6291661  
; GENERAL INFORMATION:

```
; APPLICANT: McGraw, Thomas J.
; APPLICANT: Graddis, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-12
```

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.2e-104;  
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Query Match 89.4%; Score 1110; DB 4; Length 209;  
Best Local Similarity 99.5%; Pred. No. 3e-104;  
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSDYLLQDYPYVNASNLQDEELCGGLMRVLVAQRMWERL 86  
D 1 TODCSFQHSPISSDFAVKIRELSDYFLQDYPYVNASNLQDEELCGGLMRVLVAQRMWERL 60  
QY 87 KTVAGSKMOGLLERVNTIEHFYTKCAFQPPSCLEFVOTINISRLQETSQVLAALKPWIT 146  
D 61 KTVAGSKMOGLLERVNTIEHFYTKCAFQPPSCLEFVOTINISRLQETSQVLAALKPWIT 120  
QY 147 RQNFSCLELQCCPDSSSTLPWPSPRPLEATAPTAPQPPILLLLLPVGLLLAAACLH 206  
D 121 RQNFSCLELQCCPDSSSTLPWPSPRPLEATAPTAPQPPILLLLLPVGLLLAAACLH 180  
QY 207 WQTRRRTPRPGQVPPVPSPODLLLVEH 235  
D 181 WQTRRRTPRPGQVPPVPSPODLLLVEH 209

RESULT 10  
US-09-109-100-14  
; Sequence 14, Application US/09109100C  
; Patent No. 6291661  
; GENERAL INFORMATION:  
; APPLICANT: Graddis, Thomas J.  
; APPLICANT: McGrew, Jeffrey T.  
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
; FILE REFERENCE: 03260.0028  
; CURRENT APPLICATION NUMBER: US/09/109.100C  
; CURRENT FILING DATE: 1998-07-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-109-100-14

Query Match 89.4%; Score 1110; DB 4; Length 209;  
Best Local Similarity 99.5%; Pred. No. 3e-104;  
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSDYLLQDYPYVNASNLQDEELCGGLMRVLVAQRMWERL 86  
D 1 TODCSFQHSPISSDFAVKIRELSDYLLQDYPYVNASNLQDEELCGGLMRVLVAQRMWERL 60  
QY 87 KTVAGSKMOGLLERVNTIEHFYTKCAFQPPSCLEFVOTINISRLQETSQVLAALKPWIT 146  
D 61 KTVAGSKMOGLLERVNTIEHFYTKCAFQPPSCLEFVOTINISRLQETSQVLAALKPWIT 120  
QY 147 RQNFSCLELQCCPDSSSTLPWPSPRPLEATAPTAPQPPILLLLLPVGLLLAAACLH 206  
D 121 RQNFSCLELQCCPDSSSTLPWPSPRPLEATAPTAPQPPILLLLLPVGLLLAAACLH 180  
QY 207 WQTRRRTPRPGQVPPVPSPODLLLVEH 235  
D 181 WQTRRRTPRPGQVPPVPSPODLLLVEH 209

RESULT 11  
US-09-109-100-17  
; Sequence 17, Application US/09109100C  
; Patent No. 6291661  
; GENERAL INFORMATION:  
; APPLICANT: Graddis, Thomas J.  
; APPLICANT: McGrew, Jeffrey T.  
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
; FILE REFERENCE: 03260.0028  
; CURRENT APPLICATION NUMBER: US/09/109.100C  
; CURRENT FILING DATE: 1998-07-02

; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-109-100-17

Query Match 89.4%; Score 1110; DB 4; Length 209;  
Best Local Similarity 99.5%; Pred. No. 3e-104;  
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSDYLLQDYPYVNASNLQDEELCGGLMRVLVAQRMWERL 86  
D 1 TODCSFQHSPISSDFAVKIRELSDYLLQDYPYVNASNLQDEELCGGLMRVLVAQRMWERL 60  
QY 87 KTVAGSKMOGLLERVNTIEHFYTKCAFQPPSCLEFVOTINISRLQETSQVLAALKPWIT 146  
D 61 KTVAGSKMOGLLERVNTIEHFYTKCAFQPPSCLEFVOTINISRLQETSQVLAALKPWIT 120  
QY 147 RQNFSCLELQCCPDSSSTLPWPSPRPLEATAPTAPQPPILLLLLPVGLLLAAACLH 206  
D 121 RQNFSCLELQCCPDSSSTLPWPSPRPLEATAPTAPQPPILLLLLPVGLLLAAACLH 180  
QY 207 WQTRRRTPRPGQVPPVPSPODLLLVEH 235  
D 181 WQTRRRTPRPGQVPPVPSPODLLLVEH 209

RESULT 12  
US-09-109-100-11  
; Sequence 11, Application US/09109100C  
; Patent No. 6291661  
; GENERAL INFORMATION:  
; APPLICANT: Graddis, Thomas J.  
; APPLICANT: McGrew, Jeffrey T.  
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
; FILE REFERENCE: 03260.0028  
; CURRENT APPLICATION NUMBER: US/09/109.100C  
; CURRENT FILING DATE: 1998-07-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-109-100-11

Query Match 89.2%; Score 1108; DB 4; Length 209;  
Best Local Similarity 99.5%; Pred. No. 4.8e-104;  
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSDYLLQDYPYVNASNLQDEELCGGLMRVLVAQRMWERL 86  
D 1 TODCSFQHSPISSDFAVKIRELSDYLLQDYPYVNASNLQDEELCGGLMRVLVAQRMWERL 60  
QY 87 KTVAGSKMOGLLERVNTIEHFYTKCAFQPPSCLEFVOTINISRLQETSQVLAALKPWIT 146  
D 61 KTVAGSKMOGLLERVNTIEHFYTKCAFQPPSCLEFVOTINISRLQETSQVLAALKPWIT 120  
QY 147 RQNFSCLELQCCPDSSSTLPWPSPRPLEATAPTAPQPPILLLLLPVGLLLAAACLH 206  
D 121 RQNFSCLELQCCPDSSSTLPWPSPRPLEATAPTAPQPPILLLLLPVGLLLAAACLH 180  
QY 207 WQTRRRTPRPGQVPPVPSPODLLLVEH 235  
D 181 WQTRRRTPRPGQVPPVPSPODLLLVEH 209

RESULT 13  
US-09-109-100-15  
; Sequence 15, Application US/09109100C  
; Patent No. 6291661

```
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-15
```

```
Query Match          89.2%; Score 1108; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 4.8e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 27 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPYTVASNLQDEELCGGLRWLYLAQRMWERL 86
DB 1 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPYTVASNLQDEELCGGLRWLYLAQRMWERL 60
OY 87 KTVAGSKMOGLERVTETHEIFVTKCAFQPPSCLEFVQTNISRLLOETSEQLVALKPMT 146
DB 61 KTVAGSKMOGLERVTETHEIFVTKCAFQPPSCLEFVQTNISRLLOETSEQLVALKPMT 120
OY 147 RQNFSCLELQCCPDSSITLPPWSPRPLEATAPAPPLLILLIPVGLLLAAACLA 206
DB 121 RQNFSCLELQCCPDSSITLPPWSPRPLEATAPAPPLLILLIPVGLLLAAACLA 180
OY 207 WQTRRRTPRPGQVPPVPSPODLLVEH 235
DB 181 WQTRRRTPRPGQVPPVPSPODLLVEH 209
```

```
RESULT 14
US-09-109-100-13
; Sequence 13, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-13
```

```
Query Match          89.1%; Score 1107; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 6e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 27 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPYTVASNLQDEELCGGLRWLYLAQRMWERL 86
DB 1 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPYTVASNLQDEELCGGLRWLYLAQRMWERL 60
OY 87 KTVAGSKMOGLERVTETHEIFVTKCAFQPPSCLEFVQTNISRLLOETSEQLVALKPMT 146
DB 61 KTVAGSKMOGLERVTETHEIFVTKCAFQPPSCLEFVQTNISRLLOETSEQLVALKPMT 120
OY 147 RQNFSCLELQCCPDSSITLPPWSPRPLEATAPAPPLLILLIPVGLLLAAACLA 206
DB 121 RQNFSCLELQCCPDSSITLPPWSPRPLEATAPAPPLLILLIPVGLLLAAACLA 180
OY 207 WQTRRRTPRPGQVPPVPSPODLLVEH 235
DB 181 WQTRRRTPRPGQVPPVPSPODLLVEH 209
```

```
DB 181 WQTRRRTPRPGQVPPVPSPODLLVEH 209
```

```
RESULT 15
US-09-109-100-8
; Sequence 8, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-8
```

```
Query Match          89.0%; Score 1106; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 7.6e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 27 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPYTVASNLQDEELCGGLRWLYLAQRMWERL 86
DB 1 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPYTVASNLQDEELCGGLRWLYLAQRMWERL 60
OY 87 KTVAGSKMOGLERVTETHEIFVTKCAFQPPSCLEFVQTNISRLLOETSEQLVALKPMT 146
DB 61 KTVAGSKMOGLERVTETHEIFVTKCAFQPPSCLEFVQTNISRLLOETSEQLVALKPMT 120
OY 147 RQNFSCLELQCCPDSSITLPPWSPRPLEATAPAPPLLILLIPVGLLLAAACLA 206
DB 121 RQNFSCLELQCCPDSSITLPPWSPRPLEATAPAPPLLILLIPVGLLLAAACLA 180
OY 207 WQTRRRTPRPGQVPPVPSPODLLVEH 235
DB 181 WQTRRRTPRPGQVPPVPSPODLLVEH 209
```

```
Search completed: November 24, 2002, 10:12:44
Job time : 15.1116 secs
```

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 24, 2002, 10:08:46 ; Search time 14.3755 Seconds

(without alignments)  
1544.781 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223

Sequence: 1 MTVLAPAMSPNSLLLLLL.....WQRRRRGELHPGVLPDSHP 231

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	1223	100.0	231	2	A49265 flt3/flk-2 ligand (
2	879	71.9	220	2	S43291 flt3/flk2 ligand (
3	879	71.9	220	2	I58343 flt3 ligand isoform
4	768.5	62.8	235	2	I38440 flt3 ligand - huma
5	616.5	50.4	245	2	S43293 flt3/flk2 ligand (
6	594.5	48.6	178	2	I39076 flt3 ligand alterna
7	95.5	7.8	909	1	A54809 disease resistance
8	88	7.2	843	2	T01438 hypothetical prote
9	87	7.1	291	2	AF0123 probable antigenic
10	86	7.0	962	2	C71617 SERA antigen/papai
11	85	7.0	181	2	T20323 hypothetical prote
12	84.5	6.9	939	2	E82121 peptidase, insulin
13	84	6.9	1409	2	T37188 presynaptic activi
14	83.5	6.8	552	1	A31401 macrophage colony-
15	83.5	6.8	552	1	S35703 colony-stimulat
16	83.5	6.8	2476	2	T34022 zonadhesin - pig
17	82.5	6.7	378	2	S00842 leukostallin precu
18	82.5	6.7	431	2	T04868 hypothetical prote
19	81	6.6	4131	2	T21085 hypothetical prote
20	80.5	6.6	391	2	B40892 apolipoprotein A-I
21	80.5	6.6	394	2	A25281 apolipoprotein A-I
22	80.5	6.6	395	2	A40892 apolipoprotein A-I
23	80	6.5	382	2	E84527 apolipoprotein A-I
24	79.5	6.5	399	2	T38299 apolipoprotein A-I
25	79.5	6.5	745	2	T38299 probable beta-adap
26	79	6.5	1101	2	S58108 hypothetical prote
27	78.5	6.4	122	2	D70730 hypothetical prote
28	78.5	6.4	315	2	T24821 hypothetical prote
29	78.5	6.4	379	2	T11349 ubiquinol-cytochro

30	78.5	6.4	468	2	T23091 hypothetical prote
31	78.5	6.4	3068	1	A44062 genome polyprotein
32	78	6.4	224	2	I37243 CMR-35 antigen -
33	78	6.4	743	2	T34632 probable bi-functi
34	78	6.4	806	2	E64221 phenylalanine-trna
35	78	6.4	908	2	S51293 probable membrane
36	78	6.4	1601	2	AE2011 hypothetical prote
37	78	6.4	1715	2	T06145 disease resistance
38	77.5	6.3	266	2	A45844 MHC class II histo
39	77.5	6.3	456	2	B72130 frame-shift with c
40	77.5	6.3	579	2	JC7629 membrane-type friz
41	77.5	6.3	746	2	S67203 probable membrane
42	77.5	6.3	774	2	B86492 hypothetical prote
43	77.5	6.3	774	2	H81540 hypothetical prote
44	77.5	6.3	811	2	E72003 hypothetical prote
45	77	6.3	619	2	D86509 S/T protein kinase

#### ALIGNMENTS

```
RESULT 1
A49265
flt3/flk-2 ligand precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence-revision 13-Jan-1995 #text-change 08-Oct-1999
C:Accession: A49265; I49347; I49346; S43290
R:Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, B.; Holl
D.; Williams, D.E.; Beckmann, M.P.
Cell 75, 1157-1167, 1993
A:Title: Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase receptor: a
A:Reference number: A49265; MUID:94084791; PMID:7505204
A:Accession: A49265
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-231 <IYM>
A:Cross-references: GB:I23636; NID:g439441; PIDN:AAA39436.1; PID:g439442
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.
Oncogene 11, 1165-1172, 1995
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number: I39075; MUID:96032581; PMID:7566977
A:Accession: I49347
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-163,'G',165,'HYAG' <RES>
A:Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90952.1; PID:g1072041
A:Accession: I49346
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-197,'L',198-231 <RE2>
A:Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040
R:Hannun, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.;
felt, A.; Muench, M.; Kelnier, G.; Nankkawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik
Native 368, 643-648, 1994
A:Title: Ligand for flt3/flk2 receptor tyrosine kinase regulates growth of haematopo
A:Reference number: S43290; MUID:94195428; PMID:8145851
A:Accession: S43290
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-197,'L',198-231 <HAN>
A:Experimental source: clone T110
A:Note: the sequence from Fig. 2c is inconsistent with that from Fig. 2a in having 4-
C:Genetics:
A:introns: 11/3; 49/3; 67/3; 115/3; 164/1; 224/3
C:Keywords: transmembrane protein

Query Match 100.0%; Score 1223; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.9e-101;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 61 VAVNLQDEKCKALMSFLAQRWIEQLKTVAGSKMOTLLEDVNTETHEFVTSCTFQPLPEC 120  
 |||||||  
 Db 61 VAVNLQDEKCKALMSFLAQRWIEQLKTVAGSKMOTLLEDVNTETHEFVTSCTFQPLPEC 120  
 |||||||  
 QY 121 LRFVQTNISHLKDTCTQTLALKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPLAEAT 180  
 |||||||  
 Db 121 LRFVQTNISHLKDTCTQTLALKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPLAEAT 180  
 |||||||  
 QY 181 ELPEPRRQQLLLLLLPLTVLLAAAGLWRQARRRGSLHGVPLPSHP 231  
 |||||||  
 Db 181 ELPEPRRQQLLLLLLPLTVLLAAAGLWRQARRRGSLHGVPLPSHP 231  
 |||||||

RESULT 2  
 S43291  
 FLT3/FLK2 ligand (clone T118) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 20-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 17-Mar-1999  
 C:Accession: S43291  
 R:Hanum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Ka  
 felt, A.; Muench, M.; Kelnner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A  
 Nature 368, 643-648, 1994  
 A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic  
 A:Reference number: S43290; MUID:94195428; PMID:8145851  
 A:Accession: S43291  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-220 <HAN>

Query Match 71.9%; Score 879; DB 2; Length 220;  
 Best Local Similarity 82.3%; Pred. No. 1e-70;  
 Matches 177; Conservative 5; Mismatches 21; Indels 12; Gaps 3;

QY 1 MTVLAPAMSPNSLSLLLLLSPLCLRGTPDCYFHSPISSNFKVKRELTDLKDYPT 60  
 |||||||  
 Db 1 MTVLAPAMSPNSLSLLLLLSPLCLRGTPDCYFHSPISSNFKVKRELTDLKDYPT 60  
 |||||||

QY 61 VAVNLQDEKCKALMSFLAQRWIEQLKTVAGSKMOTLLEDVNTETHEFVTSCTFQPLPEC 120  
 |||||||  
 Db 61 VAVNLQDEKCKALMSFLAQRWIEQLKTVAGSKMOTLLEDVNTETHEFVTSCTFQPLPEC 120  
 |||||||

QY 121 LRFVQTNISHLKDTCTQTLALKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRS---PLA 176  
 |||||||  
 Db 121 LRFVQTNISHLKDTCTQTLALKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRS---PLA 176  
 |||||||

QY 177 LEATELPEPRRQQLLL-----LLPLPLTVLLAA 206  
 |||||||  
 Db 178 LTATALLTVCPCGLLPLVGTSHMFPLPYFLSLSS 212  
 |||||||

RESULT 3  
 S58343  
 FLT3 ligand isoform 5H - mouse  
 C:Species: Mus sp. (mouse)  
 C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Nov-1999  
 C:Accession: J58343  
 R:Lyman, S.D.; James, L.; Escobar, S.; Downey, H.; de Vries, P.; Brasel, K.; Stocking, K  
 Oncogene 10, 149-157, 1995  
 A:Title: Identification of soluble and membrane-bound isoforms of the murine flt3 ligand  
 A:Reference number: J58343; MUID:95124710; PMID:7824267  
 A:Accession: J58343  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-220 <RES>  
 A:Cross-references: GB:S76459; NID:9913479; PIDN:AA833069.1; PID:9913480

Query Match 71.9%; Score 879; DB 2; Length 220;  
 Best Local Similarity 82.3%; Pred. No. 1e-70;  
 Matches 177; Conservative 5; Mismatches 21; Indels 12; Gaps 3;

QY 1 MTVLAPAMSPNSLSLLLLLSPLCLRGTPDCYFHSPISSNFKVKRELTDLKDYPT 60  
 |||||||

Db 1 MTVLAPAMSPNSLSLLLLLSPLCLRGTPDCYFHSPISSNFKVKRELTDLKDYPT 60  
 |||||||  
 QY 61 VAVNLQDEKCKALMSFLAQRWIEQLKTVAGSKMOTLLEDVNTETHEFVTSCTFQPLPEC 120  
 |||||||  
 Db 61 VAVNLQDEKCKALMSFLAQRWIEQLKTVAGSKMOTLLEDVNTETHEFVTSCTFQPLPEC 120  
 |||||||

QY 121 LRFVQTNISHLKDTCTQTLALKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPLAEAT 180  
 |||||||  
 Db 121 LRFVQTNISHLKDTCTQTLALKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPLAEAT 180  
 |||||||

QY 177 LEATELPEPRRQQLLL-----LLPLPLTVLLAA 206  
 |||||||  
 Db 178 LTATALLTVCPCGLLPLVGTSHMFPLPYFLSLSS 212  
 |||||||

RESULT 4  
 I38440  
 flt3 ligand - human  
 C:Species: Homo sapiens (man)  
 C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 01-Dec-2000  
 C:Accession: I38440; I39075; S43292  
 R:Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Escobar, S.S.; Downe  
 Blood 83, 2795-2801, 1994  
 A:Title: Cloning of the human homologue of the murine flt3 ligand: a growth factor fo  
 A:Reference number: I38440; MUID:94235842; PMID:8180375  
 A:Accession: I38440  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-235 <RES>  
 A:Cross-references: EMBL:U02858; NID:9494978; PIDN:AAA19825.1; PID:9494979  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-235 <RES>  
 A:Cross-references: EMBL:U02858; NID:9494978; PIDN:AAA19825.1; PID:9494979  
 R:Hanum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.;  
 felt, A.; Muench, M.; Kelnner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik  
 Nature 368, 643-648, 1994  
 A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic  
 A:Reference number: S43290; MUID:94195428; PMID:8145851  
 A:Accession: S43292  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-71, 'A', 73-235 <HAN>  
 A:Cross-references: GB:U04806; NID:9483844; PIDN:AAA17999.1; PID:9483845  
 A:Note: the authors translated the codon AGT for residue 25 as Met  
 A:Genetics: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3  
 A:Introns: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3

Query Match 62.8%; Score 768.5; DB 2; Length 235;  
 Best Local Similarity 70.3%; Pred. No. 7.1e-61;  
 Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY 1 MTVLAPAMSPNSLSLLLLLSPLCLRGTPDCYFHSPISSNFKVKRELTDLKDYPT 60  
 |||||||  
 Db 1 MTVLAPAMSP--TTVLLLLLSLSSGSGTDCSFQHSPISSDFAVKIRELSYLLQDYPVT 59  
 |||||||

QY 61 VAVNLQDEKCKALMSFLAQRWIEQLKTVAGSKMOTLLEDVNTETHEFVTSCTFQPLPEC 120  
 |||||||  
 Db 60 VASNLQDEELCGLMRLVLAQRWIEQLKTVAGSKMOTLLEDVNTETHEFVTSCTFQPLPEC 119  
 |||||||

QY 121 LRFVQTNISHLKDTCTQTLALKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPLAEAT 180  
 |||||||  
 Db 120 LRFVQTNISRLQTSQGLVALKPMWIR--QNSRCLELCQCPDSSSTLLPPWSRPLEAT 177  
 |||||||

QY 181 ELPEPRRQQLLLLLLPLTVLLAAAGLWRQARRR---GLHGVPLP 228  
 |||||||  
 Db 178 APTAPQPP--LLHLLPLVGLLLAAACLMWQTRRRTRPRGQVPVPS 227  
 |||||||

٢٤

RESULT 5  
 S43293  
 FLT3/FLT2 ligand (clone S109) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 20-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 17-Mar-1999  
 C:Accession: S43293  
 R:Hannun, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kiehl, A.; Muench, M.; Kellner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A.  
 Nature 368, 643-648, 1994  
 A:Title: Ligand for FLT3/FLT2 receptor tyrosine kinase regulates growth of haematopoietic cells  
 A:Reference number: S43290; MUID:94195428; PMID:8145851  
 A:Accession: S43293  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-245 <HMAN>  
 A:Note: the authors translated the codon AGT for residue 25 as Met

Query Match 50.48; Score 616.5; DB 2; Length 245;  
Best Local Similarity 57.08; Pred. No. 2.4e-47;  
Matches 139; Conservative 16; Mismatches 54; Indels 35; Gaps 6;

**QY** 1 MVLAPAMSPNSLLILLILLSCLRTPDCYSHPSSLNFEKVFRETDHLIKDYPVT 60  
||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :  
**Db** 1 MYLAPAMSP-ITYLIIIIIIISGLMGTCDDCSQHSPSSSDFAVKIRELSDIILQDYPT 59

QY 61 VAVNLDDEKCKALMSLEFLAQRIIEQLKVAGSKMOTLEDVNTETHFVTSCFQPLEEC 120  
|| ||||| : ||||| : ||||| ||||| ||||| ||||| |||||  
Db 60 VASNDDEELCGALWRLVLAQRMMERLKTVAGSKMOGLLERVNTETIHFVTKCAFPDPSC 119

```

09      LRFVQTINISHLTKDFTQTLALPKPCIGACQNFRCLEVCQCPDSTLLPRSPIALEAT 18
      ||||||| : : : ||| : : : ||||||| : : : ||| : : : |||
120 LRFVQTINISRLQETSEQLVALKPWITR--QNFSRCLLELQCGPGADRPQSP-GPAACGAL 176

```

```

cy 101 ELPEPRK-----KQLLELLPLPLVLAAMGLRWQRARRGEELHPGRL 227
      | | | | | | | | | | | | | | | | | | | | | | | |
Db 177 TWPRPHGEDTEAHNRGSPARCI-----AW---IQKLARGRSLPMAPL 218

```

Qy	228	PSHP	231
Db	219	IPSP	222

RESULT 6  
I39076

C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jul-2000  
C:Accession: I39076

A:Title: Structural analysis of human and murine flt3 ligand genomic loci.  
A:Reference number: 139075; MIRD:7566977  
Oncogene 11, 1165-1172, 1995

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-178 <RES>  
1:Cross-Reference: EMBL:U00074. NID:107000. EMBL:U00074.1

C:Genetics:  
A:Introns: 11/3; 48/3; 66/3; 114/3; 161/1

Best Local Similarity 73.6%; Pred. No. 1.5e-45;  
Matches 120; Conservative 14; Mismatches 26; Indels 3; Gaps 2;

```

Db      1 MIVLAPAWSP-TTYLELLLSGLSGTQDCSPQHSPISSDFAVKIRELSYLLDQYPT 59
QY      61 VAVNLODEKHCALKMSLFLAORWIEFLKTVAGSKMOTLLFDVNFTEHFWSCTEOPLDEG 120

```

Db 60 VASNDQDEELCGGLMRVLYLAQRMERLKTIVAGSKMÖGLIERVNTIEHFVTKCAFDPPSC 119

```

QY      121  LRFNQVNISHLKDTCTQTLALPKPGIGKACQNFSRCELVQCP 1633
        |||||  ::  ||:||||  :  |||||:||||
DB      120  LRFNQVNISRLQETSEQLVALKPWITR--QNFSRCELVQCP 1600

```

RESULT 7  
A54809

N:Alternate names: protein F20B18.200  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 20-Apr-2000  
C:Accession: A54908 A54911 A04354

R. Mindino, M.; Katagiri, F.; Yu, G. L.; Ausubel, F. M. Cell 78, 1089-1099, 1994

A. Title: The Arabidopsis thaliana disease resistance gene *RPS2* encodes a protein containing a leucine-rich repeat domain

A. Reference number: A54809; MIM: 65007258; PMID: 7923218

A:Accession: A54809  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-909 <MTN>

[illegible]

A:Accession: A54811  
A:Reference number: A54811; MUID:9437/9/8; PMID:8091210  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA; mRNA

A. Residues: 1-109 <EN>  
A. Cross-references: GB:014158; NID:9548085; PIDN:AAA21874.1; PID:9548086  
R. Bevan, M.; Rose, M.; Hempel, S.; Entlian, K.D.; Hohenseil, J.; Mewes, H.W.; Mayer, K.  
submitted to the Protein Sequence Database, March 1999

A/Accession: T04264  
A/Molecule type: DNA  
A/Residues: 1-909 <BEV>

A:Experimental source: cultivar Columbia; BAC clone F20B18  
C:Genetics:  
A:Gene: RPS2

A: Note: P20B18. 200  
C: Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein rep  
C: Keywords: leucine zipper; membrane protein; nucleotide binding

Query Match	7.8%;	Score 95.5;	DB 1;	Length 909;
Best Local Similarity	22.8%;	Pred. No. 2.1;		
Matches	55;	Conservative	40;	Mismatches 89; Indels 57; Gaps 11.

```

QY      14 LLLLLLLSPCLRGTPDCYFHSFSPISSEKVKFRELTD-----HLKDYPTVA----- 62
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      535 LTTLMLOQNSLKKIPGFEMHNPVLRYVLDLSPFITEIPLSIKYIVELYHLSMSGTKIS 594

```

```

QY 63 -----VNLODEKHCALMSLEL-----AQRWIEOLKIV-----AGSKMOTLLEBYNT 10
      ||: || : || | :|: : ||: ||: ||
Db 595 VLPQELGNLRKLKHLDDIQRTOQLQTIIPRDAICWLSKLEVLNLYSYAGWELQSGEGDEAE 65

```

```

QY      105 EIH-----VTSCHFOPLPECLRF--VQTNISHLKDKTCQLLALK-PCIGK 144
          1: 1      1: 1      1: 1      1: 1      1: 1      1: 1
Db      655 ELGRADLEYLENTLTIGITVLSLETCLKTLFEFGALHKHIOHLHVECCNELLYFNLPSLTN 714

```

```

QY      149  ACONFSRCLEVOQCPSSSTLBPSPILAEATELEPRPRQULLLLLLPLTVLLAAW 200
          :| | | :| | | :| | | | | | |
Db      715  HGRNLR-LSIKSCHDELYL---TPADENDWPS--LEVLTLSHLNLTIRV-----W 760

```

QY	209	G	209
Db	763	G	763

RESULT 8  
T01438  
hypothetical protein GS034D21.1 - human (fragment)

```

C:Species: Homo sapiens (man)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 05-Nov-1999
C:Accession: F01438
R:Smith, A.; Harmon, G.; Elliott, G.; Twyman, B.
submitted to the EMBL Data Library, November 1997
A:Description: The sequence of H. sapiens BAC clone GS034D21.
A:Reference number: Z4332
A:Accession: F01438
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-843 <SMT>
A:Cross-references: EMBL:AC003077; NID:g258634; PIDN:AAB83946.1; PID:g2588635
C:Genetics:
A:Map position: 7
A>Note: Intron positions not resolved (incomplete sequence)
A:Note: WUGSC:H_GS034D21.1

Query Match          7.2%, Score 88; DB 2; Length 843;
Best Local Similarity 20.1%; Pred. No. 8.8;
Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;

QY 27 GPPDGFHSPPSSAKFKFKFRELTDHLK--DYVTVAVNODCKHCKALM----SIFL 79
Db 483 GVPD-----NKSTYK-----NHMKFRDPRFHKGTK-DKDNERSKLWERTSYL 529
QY 80 AQ-----RW--TPOLKTVAGSKMOT--LLEDVNTIHF-EVTSQ-----TFQPLPECL 121
Db 530 VQSLPGISRMFEVEKREVEMSPLENALTELENNKQDLKTLISQCFQTRQMNINPLMCL 589
QY 122 -----REV 124
Db 590 NGVIDAANGVSRYOEAPEVKEYLISHPEDEGKTARLRELMLEQAQILFEGLAVHEKFEV 649
QY 125 OTNISHLLKDTCTQLLATKPCIGKACQNFRCLEVO-----CO-----PDS 165
Db 650 PQDMPLKTKVLVDQFVKKSSLG--IQEFSACMQASPVHFPNGSRVYCRNSAPASVSFDG 707
QY 166 STLPPRSPIALEA 179
Db 708 TVVIFRRSPLSYPA 721

RESULT 9
AF0123
Probable antigenic leucine-rich repeat protein YPO1006 [imported] - Yersinia pestis (stru
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AF0123
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tithball, R.W.; Holden, M.T.G.; Prentice, M.B
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Llano, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AF0123
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-291 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC89849.1; PID:g15979075; GSPDB:GN00175
C:Genetics:
A:Gene: YPO1006

Query Match          7.1%, Score 87; DB 2; Length 291;
Best Local Similarity 23.8%; Pred. No. 3.2;
Matches 50; Conservative 30; Mismatches 62; Indels 68; Gaps 11;

QY 56 DYPTVAVNODCKHCKALMSLFLAQRWLEQLKTAVG-----SKMOTLLEDVNTIHF 108
Db 24 DRPATATLTPAD--YHAIV-----EKWENDPRVYAGQRGQAVARMKECLEN-NAERLN 74
QY 109 VTSCFQQLPE-----C--LREVQTNISHL-----LKDTCTQLLATKPCIGKACQN 152
Db 75 LSSLDLSTLTPPCNBLNITCNNTLTPPTLPDNLQTLKASVQNLTPLENTPTLPASLIS 134

```

```

OY 153 FS-----RCLEVOCCDSSNLPSPSPILAA-----TCLP-----183
Db 135 LKVMNNEIERLPEPLPEGLKTLVNGC--NTSLQLPSRLPPVLESIDISNCMLTEPLPLPN 192
OY 184 -----EPRRQLLTLPLTLVLLAAW 208
Db 193 SLKELDANGNQLRLPLPLPISLRLNAVY 222

RESULT 10
C71617
SERA antigen/papain-like proteinase with active Ser PRF0345C - malaria parasite (Plas
C:Species: Plasmodium falciparum
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C:Accession: C71617
R:Gardner, M.D.; Tetteh, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.
I: Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743; PMID:9804551
A:Accession: C71617
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-962 <GAR>
A:Cross-references: GB:AE001388; GB:AE001362; NID:93845157; PIDN:AC71858.1; PID:g384
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PRF0345C
C:Superfamily: Plasmodium vivax serine-repeat antigen

Query Match 7.0%; Score 86; DB 2; Length 962;
Best Local Similarity 20.9%; Pred. No. 15;
Matches 31; Conservative 28; Mismatches 39; Indels 50; Gaps 7;

OY 8 WSPNSLLLLLLSPCLRGTPDCYFHSHPISSNF-----KYKRELTDHL-----53
Db 422 WMKNKTGLL-----PQLSYDLTYKNNNTPEFTQKSYTSQNIYDKICNHETC 470

OY 54 -LKDYPYTA-VNLQDEKHKALMSLFLAORWLEQLKTVAQSKMQLLEPVNTEHFVT 110
Db 471 NRLKDHNHCIRKIVEDOKCALNSA-FASKYHLETTIKCMG-----YEPLNASVLYVT 523

OY 111 SCTQPLPECLRFVQTNISHLKDCPTQ 138
Db 524 NC-----LKNKNKDVCTE 536

RESULT 11
T20323
hypothetical protein D1086.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T20323
R:Smye, R.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19257
A:Accession: T20323
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-181 <WIL>
A:Cross-references: EMBL:Z81491; PIDN:CAB04019.1; GSPDB:GN00023; CESP:D1086.1
A:Experimental source: clone D1086
C:Genetics:
A:Gene: CESP:D1086.1
A:Map position: 5
A:Introns: 112/3; 132/3; 167/3

Query Match 7.0%; Score 85; DB 2; Length 181;
Best Local Similarity 23.5%; Pred. No. 2.8;
Matches 39; Conservative 24; Mismatches 59; Indels 44; Gaps 8;

OY 13 SLILLLILSLCGLGTPDCYFHSHPISSNFVKRRELTDHLKD-----YPVTVAVNLQD 67

```

```

Db      8 TILPELLELSKAENSPIDSCDDLOJTVTCRKLAKLIDEMKKNPLNSGFPSEVETLN-KM 66
      68 EKHCALMSLFLAQRWTEOLKTVAGSKMOTLLEDVTEIHFVTSC---TFQPLP----- 118
      67 SGYCK-----EAMSCSPAKCPAITEKMS---KFTTKCTIDFMSGPYNQCA 111
      119 -----ECLAFVOTNISHLKD-TCTQLALAKPCI-----GKAC 150
      112 KLASNDKTECVQWYFSDKSRMSTDKCAQFAKKOCIEKDFGKAC 157

```

## RESULT 12

```

E82121
peptidase, insulinase family VC2072 [imported] - Vibrio cholerae (strain N16961 serogroup
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: E82121
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.
l., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: E82121
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-993 <HEI>
A:Cross-references: GB:AE004281; GB:AE003852; NID:g9656616; PIDN:AAF95218.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2072
A:Map position: 1
C:Superfamily: Insulysin

```

```

Query Match      6.9%: Score 84.5; DB 2; Length 939;
Best Local Similarity 24.6%: Pred No. 20;
Matches 61; Conservative 30; Mismatches 72; Indels 85; Gaps 15;

```

```

      40 SNFKVKEFRELTDHLKDY-----PVTAV-----NLQDERCKALMSLFLAQRWIEQ 86
      587 SGFSQKLPOLMEVILRKFAORDPQPKRFATIKQOMTRNNAHDKPIISOLFENATGILQ 646
      87 LKTVAGSKMOTLLEDVNTS-IEFVTSCTFO-----PLPECLAFVOTNISHLK 133
      647 PNNPPIAEALADIDYQVEFLAHFVTLISQLHVEKFTYGDMPAAEDAKH-----MAEVLK 701
      134 DTC-----TQLALAKPCI--GKACQNFSCLEVOCCQPDSSLT-----LPPRSPIAL- 177
      702 DALRVGQGTVEESLRPLVMIGKS-GTFQR--EVQCCQDDSAIVYVYQSHVSPRS-IALY 757
      178 -----EATELPEPRPROLLILL---LLPLTLIVLAAWGLRMQRARRGELHPGVP 227
      758 SLANHLMSATFFHEIRTKQOLGVMGTGMPL-----NNHFGLLT 797
      228 ----PSHP 231
      798 YVQSPSAP 805

```

## RESULT 13

```

T37188
presynaptic activity regulator aex-3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000
C:Accession: T37188
R:Imbaci, D.; Minx, M.
Submitted to the EMBL Data Library, February 1996
A:Description: The sequence of C. elegans cosmid C02H7.
A:Reference number: Z20523
A:Accession: T37188
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA

```

```

A:Residues: 1-1409 <LEI>
A:Cross-references: EMBL:049945; PIDN:AAC47926.1; GSPDB:GN00029
A:Experimental source: strain Bristol N2; clone C02H7
C:Genetics:
A:Gene: aex-3; CESP:C02H7.3
A:Map position: X:77/1, 136/2; 183/2; 232/3; 283/3; 386/3; 427/3; 527/3; 577/1; 699/3; 782/2
A:Introns: 77/1, 136/2; 183/2; 232/3; 283/3; 386/3; 427/3; 527/3; 577/1; 699/3; 782/2

```

```

Query Match      6.9%: Score 84; DB 2; Length 1409;
Best Local Similarity 23.9%: Pred. No. 36;
Matches 54; Conservative 31; Mismatches 73; Indels 68; Gaps 13;

```

```

      4 LAPANSPNSLLILLSPCGRGPDYCFSHSPRTSSNFVKFREL-TDHLKDPYPTVA 62
      317 LCPATPSE--QLLAPFPLIGVSSFFHR-----KIRLEPDSVILVLD-TNC 365
      63 VNQDERCKALMSLFL-----AQRWTEOLKTVAGSKMOTLLEDVTE----- 105
      366 LGVPD-----LYIPDLPEPDATHLKERLKN-AIKMTMTVNDNETSVTDADFGIDI 416
      106 -----IEFVTSCTFO-----TQPLPECLAFVOTNISHLKPTCTQLALAK 143
      417 DSYDVACRAVAVQFENSANVFENFSEHRTILKLYRPVAVSQDTSELSRPOCTQLIT-D 475
      144 PCIGKACQNFSCLEVOCCQPDSSLTLPPEPRSPALATELPEPRPR 188
      476 LCRTQAVEYFAEC---CLCPKNETFV--RVQAGIESAEQVGDPRK 515
      Db      476 LCRTQAVEYFAEC---CLCPKNETFV--RVQAGIESAEQVGDPRK 515

```

## RESULT 14

```

A31401
macrophage colony-stimulating factor precursor - mouse
N:Alternate names: colony-stimulating factor 1; M-CSF
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A31401; JN0294; A26575; A23166; A25883
R:Radner, M.B.; Martin, G.A.; Noble, J.A.; Wittman, V.P.; Warren, M.K.; McGrogan, M.;
Proc. Natl. Acad. Sci. U.S.A. 85, 6706-6710, 1988
A:Title: cDNA cloning and expression of murine macrophage colony-stimulating factor f
A:Reference number: A31401; MUID:88320507; PMID:2457916
A:Accession: A31401
A:Molecule type: mRNA
A:Residues: 1-552 <LAD>
A:Cross-references: GB:M21952; GB:J03862; NID:g192804; PIDN:AAA37481.1; PID:g309199
R:Harrington, M.A.; Edemberry, H.J.; Sakman, S.; Pedigo, L.M.; Daub, R.; Broxmeyer, H.
Gene 102, 165-170, 1991
A:Title: Cloning and characterization of the murine promoter for the colony-stimulat
A:Reference number: JN0294; MUID:91340149; PMID:1874443
A:Accession: JN0294
A:Molecule type: DNA
A:Residues: 1-13 <HAR>
A:Cross-references: GB:M81316; GB:M61708; NID:g192802; PIDN:AAA19866.1; PID:g192803
R:Delamarier, J.F.; Hession, C.; Semon, D.; Gough, N.M.; Rothenbuhler, R.; Mermod, J.
Nucleic Acids Res. 15, 2389-2390, 1987
A:Title: Nucleotide sequence of a cDNA encoding murine CSF-1 (macrophage-CSF).
A:Reference number: A26575; MUID:87174763; PMID:3494232
A:Accession: A26575
A:Molecule type: mRNA
A:Residues: 1-5; 'R', '7-245; 'A', 247-552 <DEU>
R:Ben-Avram, C.M.; Shively, J.E.; Shadduck, R.K.; Waheed, A.; Rajavaishisth, T.; Lusis
Proc. Natl. Acad. Sci. U.S.A. 82, 4486-4489, 1985
A:Reference number: A23166; MUID:85242709; PMID:3925458
A:Accession: A23166
A:Molecule type: protein
A:Residues: 33-39; 'CC', 42-57 <BEN>
R:Rajavaishisth, T.B.; Eng, R.; Shadduck, R.K.; Waheed, A.; Ben-Avram, C.M.; Shively,
Proc. Natl. Acad. Sci. U.S.A. 84, 1157-1161, 1987
A:Title: Cloning and tissue-specific expression of mouse macrophage colony-stimulatin
A:Reference number: A25883; MUID:87147232; PMID:3493488
A:Accession: A25883
A:Molecule type: mRNA
A:Residues: 1-2, 4-5; 'RR', 9-100 <RAJ>
A:Cross-references: GB:M15692; NID:g192800; PIDN:AAA37480.1; PID:g192801

```





GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 24, 2002, 10:03:41 ; Search time 8.42704 Seconds

(without alignments)  
1136.939 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223  
Sequence: 1 MTVLAPAMSPNSLLLLLLL.....WQRRRRGELHPGVPFSPHP 231

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1212.5	99.1	232	1	FLJL_MOUSE
2	768.5	62.8	235	1	FLJL_HUMAN
3	89.5	7.3	941	1	GBR2_HUMAN
4	89	7.3	815	1	AD15_MOUSE
5	87	7.1	816	1	AD15_RAT
6	84.5	6.9	1205	1	AT53_HUMAN
7	84	6.9	1409	1	AEX3_CAEEL
8	83.5	6.8	352	1	CSF1_MOUSE
9	83.5	6.8	2476	1	ZAN_PIG
10	82.5	6.7	378	1	LEUR_RAT
11	80.5	6.6	395	1	AP44_MOUSE
12	80	6.5	195	1	INT_OVIMO
13	79	6.5	1101	1	YNA6_SCHPO
14	78.5	6.4	122	1	YH72_MCTU
15	78.5	6.4	1208	1	RCO4_HUMAN
16	78.5	6.4	3068	1	POLG_PEMVC
17	78	6.4	224	1	CM35_HUMAN
18	78	6.4	806	1	SYFB_MYCCE
19	78	6.4	908	1	YH61_YEAST
20	77.5	6.3	266	1	HB2D_CAFNA
21	77.5	6.3	940	1	GBR2_RAT
22	76.5	6.3	222	1	YB95_MERTH
23	76.5	6.3	326	1	VS09_ROTTH
24	76.5	6.3	1296	1	ASAL_ENRFA
25	76.5	6.3	3660	1	DMD_CHICK
26	76	6.2	438	1	PR11_DROME
27	76	6.2	977	1	EP42_MOUSE
28	75.5	6.2	379	1	CYB_CAMDR
29	75.5	6.2	577	1	TRBM_MOUSE
30	75.5	6.2	4543	1	LRL1_CHICK
31	75	6.1	433	1	ENOA_SCEUN
32	75	6.1	513	1	AVR2_HUMAN
33	75	6.1	732	1	KELL_HUMAN

## ALIGNMENTS

RESULT 1	ID	FLJL_MOUSE	STANDARD	PRT	232 AA.	
AC	P49772	064085				P38435 homo sapien
DT	01-OCT-1996	(Rel. 34, Created)				P70141 rattus norv
DT	01-OCT-1996	(Rel. 34, Last sequence update)				P08406 porcine rot
DT	15-JUN-2002	(Rel. 41, Last annotation update)				P06579 bos taurus
DE	SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (Flt3 ligand) (Flt3L).					P12476 rhesus rota
GN	FLT3LG OR FLT3L.					P1855 human rotav
OS	Mus musculus (Mouse).					P12476 rhesus rota
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					P08406 porcine rot
OX	NCBI_TaxID=10090;					P12476 rhesus rota
RN	[1]					P1855 human rotav
RP	SEQUENCE FROM N.A.					P12476 rhesus rota
RA	MEDLINE=94195428; PubMed=8145851;					P08406 porcine rot
RA	Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S., Bazen J.F., Kastlein R., Hudak S., Wagner J., Mattson J., Luh J., Duda G., Martina N., Peterson D., Menon S., Shanaleit A., Muench M., Keiner G., Namikawa R., Rennick D., Roncarolo M.G., Zlotnik A., Rosnet O., Dubreuil P., Birbaumer D., Lee F.;					P12476 rhesus rota
RT	Ligand for FLT3/ELK receptor tyrosine kinase regulates growth of haematopoietic stem cells and is encoded by variant RNAs.";					P08406 porcine rot
RL	Nature 368:643-648(1994).					P12476 rhesus rota
RN	[2]					P08406 porcine rot
RP	SEQUENCE FROM N.A.					P12476 rhesus rota
RA	STRAIN=STL/J;					P08406 porcine rot
RA	MEDLINE=94084791; PubMed=7505204;					P12476 rhesus rota
RA	Lyman S.D., James L., Vandenbos T., Devries P., Brasel K., Gliniak B., Hollingsworth L.T., Picha K.S., McKenna H.J., Foxworth D., Williams D.E., Beckmann M.P.;					P08406 porcine rot
RT	Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase receptor: a proliferative factor for primitive hematopoietic cells.";					P12476 rhesus rota
RL	Cell 75:1157-1167(1993).					P08406 porcine rot
RN	[3]					P08406 porcine rot
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.					P12476 rhesus rota
RA	MEDLINE=96032581; PubMed=7566977;					P08406 porcine rot
RA	Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L., Escobar S.;					P12476 rhesus rota
RT	"Structural analysis of human and murine flt3 ligand genomic loci.";					P08406 porcine rot
RL	Oncogene 11:1165-1172(1995).					P12476 rhesus rota
RN	[4]					P08406 porcine rot
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.					P12476 rhesus rota
RA	MEDLINE=95124710; PubMed=78424267;					P08406 porcine rot
RA	Lyman S.D., James L., Escobar S., Downey H., de Vries P., Brasel K., Stocking K., Beckmann M.P., Copeland N.G., Cleveland L.S.;					P12476 rhesus rota
RT	Identification of soluble and membrane-bound isoforms of the murine flt3 ligand generated by alternative splicing of mRNAs.";					P08406 porcine rot
RL	Oncogene 10:149-157(1995).					P12476 rhesus rota
RN	[5]					P08406 porcine rot
RP	SEQUENCE FROM N.A.					P12476 rhesus rota
RA	McClanahan T., Culpepper J., Campbell D., Wagner J., Mattson J., Franz-Bacon K., Mattson J., Tsai S., Luh J., Guilmer M.J.,					P08406 porcine rot



DR Genew; HGNC:3766; FLT3LG.  
 DR MIM; 600007;  
 DR InterPro: IPR004213; FLT3\_1lg.  
 DR Pfam: PF02947; FLT3\_1lg; 1.  
 KW Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal;  
 KM 3D-structure.  
 FT SIGNAL 1 26 POTENTIAL.  
 FT CHAIN 27 235 SL CYTOKINE.  
 FT DOMAIN 27 184 EXTRACELLULAR (POTENTIAL).  
 FT TRAMEM 185 205 POTENTIAL.  
 FT DOMAIN 206 235 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 30 111  
 FT DISULFID 70 153  
 FT DISULFID 119 158  
 FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 161 178 DSDLPWSPRPRLAATA -> VETVHRVSQDGLLTS  
 FT VARSPLIC 179 235 (IN ISOFORM 2).  
 FT CONFLICT 72 72 MISSING (IN ISOFORM 2).  
 FT CONFLICT 72 72 G -> A (IN REF. 1).  
 SQ SEQUENCE 235 AA; 26416 MW; 73B95BF693B4CECF CRC64;  
 Query Match 62.8%; Score 768.5; DB 1; Length 235;  
 Best Local Similarity 70.3%; Pred. No. 2.4e-60;  
 Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;  
 QY 1 MVTYLAAPSNSLLILLLISPCLRGPPDYCFHSPISSNFKVKFRELTDHLTKDYPT 60  
 DB 1 MVTYLAAPSNSLLILLLISPCLRGPPDYCFHSPISSNFKVKFRELTDHLTKDYPT 59  
 QY 61 VAVNLDEHCKALMSFLAQRWIEOLKTVAGSKMOTLEDNTEIHFEVTSCTFQPLEEC 120  
 DB 60 VASNLODEELCGIMLVLAQRWMEKLVAGSKMGLLERNTLHFTKCAFQPPESC 119  
 QY 121 LRFVQTNISHLKDTCTQLALPKCGKACQNFSCLEYOCQDPSSTLLPPSPALAEAT 180  
 DB 120 LRFVQTNISHLKDTCTQLALPKCGKACQNFSCLEYOCQDPSSTLLPPSPALAEAT 177  
 QY 181 ELRPPRRQLLLLLPLTVILAAAGLRRQARRR---GELHGPVPLP 228  
 DB 178 APYAPPP--LLLLLPVGLLLAAAGLRRQARRR---GELHGPVPLP 227  
 RESULT 3  
 GBR2\_HUMAN STANDARD. PRT: 941 AA.  
 AC GBR2\_HUMAN STANDARD. PRT: 941 AA.  
 DT 16-OCT-2001 (Rel. 40; Created)  
 DT 16-OCT-2001 (Rel. 40; Last sequence update)  
 DT 16-OCT-2001 (Rel. 40; Last annotation update)  
 DE Gamma-aminobutyric acid type B receptor, subunit 2 precursor (GABA-B receptor 2) (GABA-B-R2) (Gb2) (GABABR2) (G protein-coupled receptor 51) (GPR 51) (HG20).  
 GN GABABR2 OR GPR51.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A. (ISOFORM 2A).  
 RC TISSUE=Cerebellum;  
 RX MEDLINE=99087321; PubMed=9872316;  
 RA White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H., Barnes A.A., Emson P., Ford S.M., Marshall F.H.;  
 RT "Heterodimerization is required for the formation of a functional GABA(B) receptor.";  
 RT Nature 396:679-682(1998).  
 RN [2]  
 RN PARTIAL SEQUENCE FROM N.A. (ISOFORMS 2A; 2B AND 2C).  
 RC TISSUE=Brain;  
 RX MEDLINE=20193514; PubMed=10727622;  
 RA Clark J.A., Mezey E., Lam A.S., Bonner T.I.;  
 RT "Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";

RL Brain Res. 860:41-52(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 2A).  
 RA Liu M., Parker R., McCrea K., Watson J., Baker E., Sutherland G., Herzog H.;  
 RT "Cloning and characterization of a novel human GABA-B receptor subtype with high affinity for GABA and low affinity for baclofen.";  
 RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 2A).  
 RC TISSUE=Hippocampus;  
 RA Borowsky B., Laz T., Gerald C.;  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 2A).  
 RC TISSUE=Retal brain;  
 RX MEDLINE=99189236; PubMed=10087195;  
 RA Ng G.Y.K., McDonald T., Bonner T., Rigby M., Heavens R., Whiting P., Chateauf A., Coulombe N., Kargman S., Caskey T., Evans J.F., O'Neill G.P., Liu Q.;  
 RT "Cloning of a novel G-protein-coupled receptor GPR 51 resembling GABAB receptors expressed predominantly in nervous tissues and mapped proximal to the hereditary sensory neuropathy type 1 locus on chromosome 9.";  
 RT Genomics 56:288-295(1999).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 2A), AND VARIANTS PHE-628 AND ALA-869.  
 RC TISSUE=Brain;  
 RX MEDLINE=99263199; PubMed=10328880;  
 RA Martin S.C., Russek S.J., Farb D.H.;  
 RT "Molecular identification of the human GABABR2: cell surface expression and coupling to adenylyl cyclase in the absence of GABABR1.";  
 RT Mol. Cell. Neurosci. 13:180-191(1999).  
 RN [7]  
 RP RIA-R2 INTERACTION.  
 RX MEDLINE=99175124; PubMed=10075644;  
 RA Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan R., Kargman S., Chateauf A., Tsukamoto N., McDonald T., Whiting P., Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F., Bonner T.I., O'Neill G.P.;  
 RT "Identification of a GABAB receptor subunit, gb2, regulated for functional GABAB receptor activity.";  
 RT J. Biol. Chem. 274:7607-7610(1999).  
 RN [8]  
 RP RIA-R2 INTERACTION.  
 RX MEDLINE=20237752; PubMed=10773016;  
 RA Sullivan R., Chateauf A., Coulombe N., Kolakowski L.F. Jr., Johnson M.P., Hebert T.E., Ethier N., Belle M., Welters K., Abramowitz M., O'Neill G.P., Ng G.Y.K.;  
 RT "Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B)) receptors with truncated receptors and metabotropic glutamate receptor 4 supports the GABA(B) heterodimer as the functional receptor.";  
 RT J. Pharmacol. Exp. Ther. 293:460-467(2000).  
 RN [9]  
 RP FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY, STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS, INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES INOSTOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND ANTINOCICEPTION.  
 CC -1- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO HAPPEN.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER

CC		COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
CC		PREEXISTING SITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
CC		PLASMA MEMBRANE.
CC	-I-	ALTERNATIVE PRODUCTS. 3 ISOFORMS; 2A (SHOWN HERE), 2B AND 2C; ARE
CC		PRODUCED BY ALTERNATIVE SPLICING.
CC	-I-	TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN
CC		CEREBRAL CORTEX, THALAMUS, HIPPOCAMPI, FRONTAL, OCCIPITAL AND
CC		TEMPORAL LOBE, OCCIPITAL POLE AND CEREbellUM, FOLLOWED BY CORPUS
CC		CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, AMYGDALA AND MEDULLA.
CC	-I-	WEAKLY EXPRESSED IN HEART, TESTIS AND SKELETAL MUSCLE.
CC	-I-	DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
CC		MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.
CC	-I-	SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC		GABA-B RECEPTOR SUBFAMILY.
CC		-----
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration
CC		between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC		the European Bioinformatics Institute. There are no restrictions on its
CC		use by non-profit institutions as long as their content is in no way
CC		modified and this statement is not removed. Usage by and for commercial
CC		entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>
CC		or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC		-----
DR	EMBL:	AJ012188: CAO9942.1; -
DR	EMBL:	AF056085: AAC63228.1; -
DR	EMBL:	AF095723: AAC63383.1; -
DR	EMBL:	AF095724: AAC63384.1; -
DR	EMBL:	AF095784: AAD30389.1; -
DR	EMBL:	AF074483: AAD03346.1; -
DR	EMBL:	AF069755: AAC99345.1; -
DR	EMBL:	AF098033: AAD45867.1; -
DR	Genew:	HGNC:4507; GPR51.
DR	InterPro:	IPR001828; ANF_receptor.
DR	Interpro:	IPIR000337; GPCR_Mgr.
DR	Pfam:	PF000003; 7tm_3; 1.
DR	Pfam:	PF01094; ANF_receptor; 1.
DR	PROSITE:	PS00979; G_PROTEIN_REC_P3.1; FALSE_NEG.
DR	PROSITE:	PS00980; G_PROTEIN_REC_P3.2; FALSE_NEG.
DR	PROSITE:	PS00981; G_PROTEIN_REC_P3.3; FALSE_NEG.
DR	PROSITE:	PS0259; G_PROTEIN_REC_P3.4; 1.
KM		G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW		Postsynaptic membrane; Coiled coil; Alternative splicing;
KW		Polymorphism.
FT	CHAIN	1 41 POTENTIAL.
FT		GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR,
FT		SUBUNIT 2.
FT	DOMAIN	42 483 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	484 504 I (POTENTIAL).
FT	DOMAIN	505 522 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	523 543 II (POTENTIAL).
FT	DOMAIN	544 551 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	552 572 III POTENTIAL.
FT	DOMAIN	573 597 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	598 618 IV (POTENTIAL).
FT	DOMAIN	619 654 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	655 675 V (POTENTIAL).
FT	DOMAIN	676 691 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	692 712 VI (POTENTIAL).
FT	DOMAIN	713 720 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	721 741 VII (POTENTIAL).
FT	DOMAIN	742 941 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	743 819 COILED COIL (POTENTIAL).
FT	DOMAIN	820 900 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	901 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	299 389 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	390 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	405 453 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	454 927 MISSING (IN ISOFORM 2B).
FT	VARSPLIC	928 941 HIVSFVMTSGSL -> TITLGRCVCNNTVSGCGAGHHG
FT	WPLETTETMALRWGRGRGLGT (IN ISOFORM 2C).	
FT	Y -> F.	
FT	Variant	628 628
FT	Variant	
FT	Variant	869 869
FT	Variant	T -> A.
FT	Variant	/FTID=VAR_010148.

FT	CONFLICT	6	6	/FTID=VAR.010149.					
FT	CONFLICT	12	12	S -> R (IN REF. 5).					
FT	CONFLICT	424	424	P -> R (IN REF. 5).					
FT	CONFLICT	941 AA:	105821 MW:	G -> E (IN REF. 3).					
SEQ	SEQUENCE			09F1773DB0673C5D	CRC64;				
Query Match									
Best Local Similarity		7.3%: Score 89.5; DB 1;		Length 941;					
Matches		24; Conservative		Pred. No. 3.3;					
		0; Mismatches		16; Indels					
				9; Gaps					
QY	183 PEPRRQILLILLPLPITVILAAWGLRWGRARRRGELHPCVLPSPH 231								
DB	15 PPPPPARLLILLPLPLPLAPAGWG--WARGAPR-----PPSP 54								
RESULT 4									
ID	AD15_MOUSE	STANDARD:	PRT:	815 AA.					
AC	088839; g9qyL2;								
DT	16-OCT-2001 (Rel. 40, Created)								
DT	16-OCT-2001 (Rel. 40, Last sequence update)								
DT	15-JUN-2002 (Rel. 41, Last annotation update)								
DE	ADAM 15 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase domain 15) (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein 15) (MDC-15) (Metalloproteinase RGD disintegrin protein) (Metargidin) (AD56).								
DE	ADAM15 OR MDC15.								
GN	Mus musculus (Mouse).								
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
OX	NCBI_TaxID=10090;								
RN	[1]								
RP	SEQUENCE FROM N.A. AND PROCESSING.								
RC	TISSUE=Lung;								
RX	MEDLINE=98421554; PubMed=9748307;								
RA	Lum L., Reid M.S., Blobel C.P.;								
RT	"Intracellular maturation of the mouse metalloproteinase disintegrin MDC15.";								
RL	J. Biol. Chem. 273:26236-26247(1998).								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Myeloid; and Myeloma;								
RA	Shimizu E., Higuchi Y., Matsuura K., Hijiya N., Yamamoto S.;								
RL	Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.								
RN	[3]								
RP	INTERACTIONS WITH ENDOPHILIN I AND SORTING NEXIN 9.								
RX	MEDLINE=20002705; PubMed=1053137;								
RA	Howard L., Nelson R.K., Mciewicz R.A., Blobel C.P.;								
RL	"Interaction of the metalloproteinase disintegrins MDC9 and MDC15 with the SH3 domain-containing proteins, endophilin I and SHP3X1.";								
CC	J. Biol. Chem. 274:31693-31699(1999).								
CC	-1- FUNCTION: MAY BE INVOLVED IN CELL-SURFACE PROTEOLYSIS, CELL ADHESION OR INTRACELLULAR PROTEIN MATURATION.								
CC	-1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).								
CC	-1- SUBUNIT: INTERACTS WITH INTEGRIN ALPHA-V-BETA3, ENDOPHILIN I AND SORTING NEXIN 9. ENDOPHILIN I AND SORTING NEXIN 9 PREFERENTIALLY BIND THE PRECURSOR BUT NOT THE PROCESSED FORM OF ADAM15, SUGGESTING THAT THE INTERACTION OCCURS IN A SECRETORY PATHWAY COMPARTMENT PRIOR TO THE MEDIAL GOLGI.								
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE MAJORITY OF THE PROTEIN IS LOCALIZED IN A PERINUCLEAR COMPARTMENT WHICH MAY CORRESPOND TO THE TRANS-GOLGI NETWORK OR THE LATE ENDOSOME. THE PRO-PROTEIN IS THE MAJOR DETECTABLE FORM ON THE CELL SURFACE, WHEREAS THE MAJORITY OF THE PROTEIN IN THE CELL IS PROCESSED.								
CC	-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, BRAIN, LUNG, AND KIDNEY. EXPRESSED AT LOWER LEVELS IN SPLEEN, LIVER, TESTIS AND MUSCLE.								
CC	-1- DOMAIN: THE CYTOPLASMIC DOMAIN INTERACTS WITH ENDOPHILIN I AND SORTING NEXIN 9.								
CC	-1- DOMAIN: DESINTEGRIN DOMAIN BINDS TO INTEGRIN ALPHA-V-BETA3 (BY SIMILARITY).								
CC	-1- PTM: THE PRECURSOR IS CLEAVED BY A FUZIN ENDOPEPTIDASE. AN								

ADDITIONAL MEMBRANE PROXIMAL SITE OF CLEAVAGE AFFECTS A SMALL PERCENTAGE OF THE PROTEIN AND RESULTS IN DISULFIDE-LINKED FRAGMENTS. THE PRO-DOMAIN IS APPARENTLY CLEAVED IN SEVERAL POSITIONS THAT ARE N-TERMINAL OF THE FIRIN CLEAVAGE SITE.

-1- PFM: MAY BE PARTIALLY SIALYLATED.

-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.

-1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

-1- SIMILARITY: CONTAINS 1 DISINTEGRIN DOMAIN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb.ch/announce/or send an email to license@isb-sib.ch>).

CC -----

DR EMBL: AF006196; AAC61896.1; -

DR EMBL: AB022089; BAA88903.1; -

DR HSSP: P17494; 1KST.

DR MEROPS: M12.215; -

DR MGD: MGI:133382; Adam15.

DR InterPro: IPR001762; Disintegrin.

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR001818; Matrxin.

DR InterPro: IPR002870; Pep\_M12B\_propep.

DR InterPro: IPR001590; Repolysin.

DR InterPro: IPR000130; Zn\_MPeptidase.

DR Pfam: PF00200; disintegrin.1.

DR Pfam: PF01421; Repolysin.1.

DR Pfam: PF01562; Pep\_M12B\_propep.1.

DR Pfam: PD000664; Disintegrin.1.

DR SMART: SM00181; EGF.1.

DR SMART: SM00181; EGF.1.

DR PROSITE: PS00022; EGF\_1; FALSE\_NEG.

DR PROSITE: PS00022; EGF\_1; FALSE\_NEG.

DR PROSITE: PS01186; EGF\_2.1.

DR PROSITE: PS00427; DISINTEGRIN\_1; FALSE\_NEG.

DR PROSITE: PS00427; DISINTEGRIN\_2; 1.

DR PROSITE: PS00142; ZINC\_PROTEASE.1.

DR PROSITE: PS00546; CYSTEINE\_SWITCH; FALSE\_NEG.

KM Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;

Transmembrane; EGF-like domain; SH3-binding.

FT SIGNAL 1 17

FT PROPEP 18 207

FT CHAIN 208 815

FT DOMAIN 208 696

FT TRANSMEM 697 717

FT DOMAIN 718 815

FT DOMAIN 208 415

FT DOMAIN 422 509

FT DOMAIN 510 657

FT DOMAIN 658 686

FT DOMAIN 699 712

FT SITE 767 773

FT SITE 802 808

FT SITE 179 179

FT SITE 287 288

FT METAL 349 349

FT METAL 350 350

FT ACT\_SITE 350 353

FT METAL 353 353

FT METAL 359 359

FT METAL 324 410

FT DISULFID 481 494

FT DISULFID 658 668

FT DISULFID 662 674

FT DISULFID 676 685

FT CARBOHYD 238 238

FT CARBOHYD 390 390

FT CARBOHYD 393 393

FT CARBOHYD 607 607

FT CARBOHYD 612 612

FT CONFLICT 21 22

PP -> RR (IN REF. 2).

FT CONFLICT 443 443 E -> Q (IN REF. 2).

FT CONFLICT 459 459 G -> E (IN REF. 2).

FT CONFLICT 564 565 SP -> T (IN REF. 2).

FT CONFLICT 654 654 G -> E (IN REF. 2).

FT CONFLICT 660 660 R -> S (IN REF. 2).

FT CONFLICT 703 703 L -> R (IN REF. 2).

FT CONFLICT 712 712 L -> R (IN REF. 2).

FT CONFLICT 729 729 L -> R (IN REF. 2).

FT CONFLICT 797 797 L -> S (IN REF. 2).

FT CONFLICT 803 805 PAP -> AAS (IN REF. 2).

FT CONFLICT 810 810 A -> P (IN REF. 2).

SO SEQUENCE 815 AA; 87424 MW; C064BD3B7347D19B CRG64;

Query Match 7.38; Score 89; DB 1; Length 815;

Best Local Similarity 23.7%; Pred. No. 3.2;

Matches 52; Conservative 13; Mismatches 56; Indels 98; Gaps 9;

QY 69 KHKALMSLFLAQWIMQKLVAGSKMOTLEDVNTIHFVTSCTPP-----LP----- 118

Db 530 KQCSLWG-----PGAPAPAPLCLQANTINGAMFGSCGSGSYPCAPRDY 577

QY 119 -----EC-----LRFVQTNISHLKDTCTQ-----LLALK----- 143

Db 578 MCGQLQCGWGRSPPLDLSYQDRLESEVLEANGTOLNCSWVDLIGNVAPLALPFTAG 637

QY 144 ---PCIGKACQ-----NSRCLEVOCPDSSTLPPSPIAL 177

Db 638 PGLVCIQHRCQPVLDLGAQECRRKCHGVODSSGHCCEGMAPDQMQLKATSLT 697

QY 178 EATLEPRPRQLLLLLPLTVLLAAMGLMORAR 216

Db 698 G-----LLLSLLLVLLVLLGAST---WHRAR 721

RESULT 5

AD15\_RAT STANDARD; PRT; 816 AA.

ID AD15\_RAT

AC Q9QYV0;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE ADM15 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase domain 15) (metalloproteinase-like, disintegrin-like, and cysteine-rich protein 15) (MDC-15) (Metalloprotease RGD disintegrin protein)

DE rich protein 15)

DE (Metargidin) (CRII-7).

DE ADAM15 OR MDC15.

GN ADAM15 OR MDC15.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI\_TaxID=10116;

[1]

RP SEQUENCE FROM N.A.

RC TISSUE-Sciatic nerve;

RX MEDLINE=20556183; PubMed=11102971;

RA Bosse F., Petzold G., Greiner-Petter R., Pippl U., Gillen C., Mueller H.-W.;

RT "Cellular localization of the disintegrin CRII-7/rMDC15 mRNA in rat PNS and CNS and regulated expression in postnatal development and after nerve injury";

RL Gila 32:313-327(2000).

CC -1- FUNCTION: MAY BE INVOLVED IN CELL-SURFACE PROTEOLYSIS, CELL ADHESION OR INTRACELLULAR PROTEIN MATURATION.

CC -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

CC -1- SUBUNIT: INTERACTS WITH INTEGRIN ALPHA5-BETA3, ENDOPHILIN I AND SORTING NEXIN 9. ENDOPHILIN I AND SORTING NEXIN 9 PREFERENTIALLY BIND THE PRECURSOR BUT NOT THE PROCESSED FORM OF ADAM15, SUGGESTING THAT THE INTERACTION OCCURS IN A SECRETORY PATHWAY COMPARTMENT PRIOR TO THE MEDIAL GOLGI (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: TYPE I membrane protein.

CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN, SPINAL CORD, SCIATIC NERVE AND LUNG. EXPRESSED AT LOWER LEVELS IN ALL OTHERS TISSUES. IN THE PERIPHERAL NERVOUS SYSTEM, EXPRESSED PREDOMINANTLY BY SCHWANN CELLS. IN THE CENTRAL NERVOUS SYSTEM, PREFERENTIALLY

```

SQ      SEQUENCE      816 AA; 88051 MW; B9D2CE023266FC27 CRC64;
Query Match      7.1%; Score 87; DB 1; Length 816;
Best Local Similarity 22.6%; Pred. No. 4.7;
Matches 62; Conservative 18; Mismatches 58; Indels 136; Gaps 13;

QY      69      KKKCALMSLFLAQWRIEOLKTVAGSKMOTLLEDVETVETIHFTSCMPOP-----LP----- 118
DB      531      RCGOSLIMG-----PEAQPAALCLQIQTANTKGNAGSCGRSPSGSYMCNLRDA 578
QY      119      -----EC-----LRFVQTNISHLKDTCTQ-----LALKPCIGK 148
DB      579      ICGLOCCGWRNQPLIGSVQDQLSEVLBANGTLCMCSWVDLDGNDVAQPLALP---GT 635
QY      149      AAGNPSRCLEVOCP-----DST-----LPPSPIALEXTEL 162
DB      636      ACGPGLVTCIGHGCPVDLLGAOECSKCHGVCDSSNRHCHDEGMAPPCDMOLRATS- 694
QY      183      PEPRPRPOL-----LILLILLPLTLLVLLAAMWGGRMORAR----- 216
DB      695      -----SLTGLLSLLILLIVLVLLGASY---WYRARLHQRLCOLKSSCOYRAAGSGPP 745
QY      217      -----RKGELHPGV-----PLPSHP 231
DB      746      ERPGPORAQOMPZTKPGQPTKPPPKPLPANP 779

RESULT 6
AT53_HUMAN
ID      AT53_HUMAN      STANDARD; PRT; 1205 AA.
AC      015072; Q9BXZ8;
DT      16-OCT-2001 (Rel. 40, Created)
DF      15-JUN-2002 (Rel. 41, Last sequence update)
DE      15-JUN-2002 (Rel. 41, Last annotation update)
AD      ADAMTS-3 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase
DE      with thrombospondin motifs 3) (ADAM-TS 3) (ADAM-TS3) (Procollagen II
DE      amino-propeptide processing enzyme) (Procollagen II N-proteinase) (PC
DE      II-NP).
GN      ADAMTS3 OR KIAA0365.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE OF 1-227 FROM N.A.
RA      MEDLINE=21402912; PubMed=11408482;
RX      Fernandes R.J., Hirohata S., Engle J.M., Collige A., Cohn D.H.,
RA      Eyre D.R., Apte S.S.;
RT      "Procollagen II amino propeptide processing by ADAMTS-3. Insights on
RT      dermatosparaxis."
RL      J Biol. Chem. 276.31502-31509(2001).
RN      [2]
RP      SEQUENCE OF 5-1205 FROM N.A.
RA      TISSUE=Brain;
RX      MEDLINE=97349984; PubMed=9205841;
RA      Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
RA      Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT      "Prediction of the coding sequences of unidentified human genes. VII.
RT      The complete sequences of 100 new cDNA clones from brain which can
RT      code for large proteins in vitro."
RL      DNA Res. 4:141-150(1997).
CC      -1- FUNCTION: cleaves the propeptides of type II collagen prior to
CC      fibril assembly. Does not act on types I and III collagens.
CC      -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
CC      matrix (By similarity).
CC      -1- TISSUE SPECIFICITY: Found in cartilage and skin.
CC      -1- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
CC      FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
CC      -1- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
CC      SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
CC      -1- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN

```

```

CC -1- SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.
CC -1- CAUTION: HAS SOMETIMES BEEN REFERRED TO ADAMTS4.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF247668; AAK28400.1; -.
CC EMBL; AB002364; BAA20821.1; -.
CC MEROPS; M12.220; -.
CC Genew; HGNC:219; ADAMTS3.
CC MIM; 605011; -.
CC InterPro; IPR001762; Disintegrin.
CC InterPro; IPR002870; Pep_M12B_propep.
CC InterPro; IPR001590; Reprolysin.
CC InterPro; IPR000884; TSP1.
CC InterPro; IPR000130; Zn_MTPeptide.
CC Pfam; PF00090; tsp_1; 4.
CC Pfam; PF01421; Reprolysin; 1.
CC Pfam; PF01562; Pep_M12B_propep; 1.
CC SMART; SM00209; TSP1; 4.
CC PROSITE; PS50215; ADAM_MEROPS; 1.
CC PROSITE; PS00142; ZINC_PROTEASE; FALSE NEG.
CC PROSITE; PS00427; DISINTEGRIN_1; FALSE NEG.
CC HydroLase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
CC Repeat; Extracellular matrix; Heparin-binding.
CC K1 SIGNAL 1 20
CC FT PROPEP 21 249 BY SIMILARITY.
CC FT CHAIN 250 1205 ADAMTS-3.
CC FT METAL 398 398 ZINC (CATALYTIC) (BY SIMILARITY).
CC FT ACT_SITE 399 399 BY SIMILARITY.
CC FT METAL 402 402 ZINC (CATALYTIC) (BY SIMILARITY).
CC FT METAL 408 408 ZINC (CATALYTIC) (BY SIMILARITY).
CC FT DOMAIN 470 550 ZINC (CATALYTIC) (BY SIMILARITY).
CC FT DOMAIN 551 607 DISINTEGRIN-LIKE.
CC FT DOMAIN 657 657 TSP TYPE-1 1.
CC FT DOMAIN 712 712 CYS-RICH.
CC FT DOMAIN 713 844 SPACER.
CC FT DOMAIN 845 902 TSP TYPE-1 2.
CC FT DOMAIN 903 965 TSP TYPE-1 3.
CC FT DOMAIN 966 1017 TSP TYPE-1 4.
CC FT DOMAIN 246 249 POLY-ARG.
CC FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 345 345 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 942 942 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SO SEQUENCE 1205 AA; 135570 MW; EB07B286FC85FB87 CRC64;

Query Match 6.9%; Score 84.5; DB 1; Length 1205;
Best Local Similarity 21.9%; Pred. No. 12;
Matches 49; Conservative 22; Mismatches 80; Indels 73; Gaps 10

40 SNFVFRRELTDLRLDYPTVAVNLODERHCKALMSFLAORMIEOLKTYAGSR----- 94
   1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:
Db 876 SDNKMYHRSFCEANKRPKPIRRCNINIOECTH-----PLVAEEWHCHCTKTCGSSGYQLRT 930
   1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:

95 -----MOTLLEVDNTEHFV-----TSCIFQQLP-----DELKRV--QTNISH 130
   1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:

931 VRCLQPLLDITNSKVSYSKCMGDRPESRRPCRRVPCPAQMKKTGWSECSVTGCGEIVRQ 990
   1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:

131 LL-----WDCTQLLALKPCIGKAC-----QNFRCLEVOG 161
   1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:

991 VLCAAGHCHCGEKPESTRACQLPQNDDECLDKSIFCOMEYLARCYSPENYKLCESC 1050
   1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:

162 QPDSSTLLPRPSRLALEATEL-----PEPRROLILLILLP 198
   1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:

```

[illegible]



```
Db 366 LQVDD-----LXIPDLPEPDATHLKERLKN-AINKMTMTVDNETSVTDADFGIDI 416
Oy 106 -----IHPVTSC-----TFQPLPECLARVCYNINISHLKDTCTQLLAK 143
Db 417 DSDVADVACRVAVQPFNSANWFGNSEHTRTLRLYPRPVSLQDLSFLRSPQCTOLIT-D 475
Oy 144 PCIGKACQNSFCLEWQCO-PDSSTLLPPRSPALENTELEPPRPR 188
Db 476 LCRTQAVEYFAEC-----CLCPKNETFV--RVQAGIESAEQVGDKPK 515

RESULT 8
CSF1_MOUSE
ID CSF1_MOUSE STANDARD: PRT; 552 AA.
AC P07141;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Macrophage colony stimulating factor-1 precursor (CSF-1) (MCSF).
GN CSF1 OR CSF1.
OS Mus musculus (Mouse), and
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090, 10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse;
RX MEDLINE=87174763; PubMed=3494232;
RA Delamarier J.F., Hession C., Semon D., Gough N.M., Rothenbuhler R.,
RT Mermod J.-J.;
RL "Nucleotide sequence of a cDNA encoding murine CSF-1
   (Macrophage-CSF).";
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse;
RX MEDLINE=88320507; PubMed=2457916;
RA Lader M.B., Martin G.A., Noble J.A., Wiltman V.P., Warren M.K.,
RT McGrogan M., Stanley E.R.;
RL "CDNA cloning and expression of murine macrophage colony-stimulating
   factor from 1929 cells.";
RN [3]
RP SEQUENCE OF 1-100 FROM N.A.
RC SPECIES=Mouse;
RX MEDLINE=87147232; PubMed=3493488;
RA Rajavashisth T.B., Eng R., Shaddock R.K., Waheed A., Ben-Avram C.M.,
RT Shively J.E., Lusis A.J.;
RL "Cloning and tissue-specific expression of mouse macrophage colony-
   stimulating factor mRNA.";
RN [4]
RP SEQUENCE OF 33-57.
RC SPECIES=Mouse;
RX MEDLINE=85242709; PubMed=3925458;
RA Ben-Avram C.M., Shively J.E., Shaddock R.K., Waheed A.,
RT Rajavashisth T.B., Lusis A.J.;
RL "Amino-terminal amino acid sequence of murine colony-stimulating
   factor 1.";
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse;
RX MEDLINE=93363632; PubMed=8357831;
RA Borycki A.G., Lenormand J., Guillier M., Leibovitch S.A.;
RT "Isolation and characterization of a cDNA clone encoding for rat
   CSF-1 gene. Post-transcriptional repression occurs in myogenic
   differentiation.";
RL Biochim. Biophys. Acta 1174:143-152(1993).
RN [6]
RP SEQUENCE OF 1-13 FROM N.A.
```

```
RC SPECIES=Mouse;
RX MEDLINE=91340149; PubMed=1874443;
RA Harrington M.A., Edenberg H.J., Saxman S.M., Pedigo L.M., Daub R.,
RT Broyde M.E.;
RL "Cloning and characterization of the murine promoter for the colony-
   stimulating factor-1 encoding gene.";
RN [1]
RP FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
   CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
   DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
   OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES.
CC -I- SUBUNIT: HOMODIMER, LINKED BY THREE DISULFIDE BONDS.
CC -I- FUNCTION: THIS CSF INDUCES MACROPHAGES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X05010; CAA28660.1; -
DR EMBL; M21952; AAA37481.1; -
DR EMBL; M21149; AAA37482.1; -
DR EMBL; M15692; AAA37480.1; -
DR EMBL; M84361; AAA30303.1; -
DR EMBL; M81316; AAA19866.1; -
DR PIR; A23166; A23166;
DR PIR; A26575; A26575;
DR PIR; A31401; A31401;
DR MGD; MGI:1339753; Csfl.
KW Cytokine; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1
FT CHAIN 33
FT DISULFID 63
FT DISULFID 63
FT DISULFID 39
FT DISULFID 80
FT DISULFID 134
FT DISULFID 189
FT DISULFID 191
FT CARBOHYD 107
FT CARBOHYD 154
FT CARBOHYD 172
FT VARIANT 292
FT VARIANT 345
FT CONFLICT 3
FT CONFLICT 6
FT CONFLICT 7
FT CONFLICT 246
SQ SEQUENCE 552 AA; 60648 MW; 3886D72D0E770AF CRC64;

Query Match 6.8%; Score 83.5; DB 1; Length 552;
Best Local Similarity 23.2%; Pred. No. 6.2;
Matches 54; Conservative 36; Mismatches 94; Indels 49; Gaps 12;

Oy 12 SLLILLLSPCLRGPDGCFSHSPSSNFKYKFEILDHLKDPVYVAVNLQDEKH- 70
Db 18 SRLILVLLMSRSIAKEVSEHSCSHMIGNHLY- LQDLIDSQN-ETSCQIAFEVYQDEOL 75
Oy 71 ----CKALMSLFLAQRVTEOL-----KTVGSKMQTLLEEDVNTIEHFVTSCTFOPAP 118
Db 76 DDPVCYLKRAFLVQDIDETMRFKONTPRANITERLQELSNLN-----SCFKQYE 128
Oy 119 E-----CLR-FVQF-----NISHLKDTCTQLALPCIGKACQNSFCSC-LEWQCOOPD 164
Db 129 EQNKACVRFTHETPLQLEIKNFENETKNLLEKDMNIFTKKCNNSFAKCSSRDVVTKPD 188
Oy 165 SSTLLPPRSPALENTELEPPRROLILLILPLTLVLAAWGIKRWGRARR 217
Db 189 CNCLYPRATPSSDPFASAPQPPAP-----SWAPLA-----GLAWDSOR 228
```



RESULT 9  
ZAN\_PIG STANDARD: PRT: 2476 AA.  
ID ZAN\_PIG  
AC 028983;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Zonadhesin precursor.  
GN ZAN.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxId=9823;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 823-830; 859-872; 883-890;  
RP 920-925; 960-967; 1235-1244; 1349-1354; 1518-1532; 1624-1656;  
RP 1658-1667; 1777-1795 AND 1914-1921.  
RC STRAIN=Weishan; TISSUE=Testis;  
RA MEDLINE=96064658; PubMed=7592795;  
RA Hardy D.M., Garbers D.L.;  
RT "A sperm membrane protein that binds in a species-specific manner to  
RT the egg extracellular matrix is homologous to von Willebrand  
RT factor";  
RL J. Biol. Chem. 270:26025-26028(1995).  
CC -1- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA  
CC OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR  
CC SIGNALING.  
CC -1- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE  
CC APICAL REGION OF THE SPERM HEAD (BY SIMILARITY).  
CC -1- TISSUE SPECIFICITY: IN TESTIS, PRIMARILY IN HARPOID SPERMATIDS.  
CC NOT IN LUNG, LIVER, HEART, SPLEEN, BRAIN, KIDNEY, EPIDIDYMS.  
CC -1- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE  
CC ZONA PELLUCIDA.  
CC -1- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS,  
CC THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF  
CC SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.  
CC -1- DOMAIN: THE WVD DOMAINS 2 AND 3 MAY MEDIATE COVALENT  
CC OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).  
CC -1- PTM: THE MAM DOMAINS AND THE MUCIN-LIKE DOMAINS ARE MISSING  
CC FROM THE ZONADHESIN THAT BINDS TO THE EGG EXTRACELLULAR MATRIX.  
CC PROCESSING MIGHT OCCUR DURING SPERM MATURATION AND/OR  
CC CAPACITATION.  
CC -1- SIMILARITY: CONTAINS 2 MAM DOMAINS.  
CC -1- SIMILARITY: CONTAINS 4.5 WVD DOMAINS.  
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.  
CC -----  
CC This SMS-S-PROF entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
CC EMBL: U40024; AAC48486.1; -.  
DR HSSP: P56682; ICSV.  
DR InterPro: IPR000561; EGF-like.  
DR InterPro: IPR000998; MAM\_domain.  
DR InterPro: IPR002919; TIL\_Cysrich.  
DR InterPro: IPR003328; TILa\_Cysrich.  
DR InterPro: IPR001007; WVF\_C.  
DR InterPro: IPR001846; WVF\_D.  
DR Pfam: PF00094; vwd; 4.  
DR Pfam: PF00629; MAM; 2.  
DR Pfam: PF01826; TIL; 5.  
DR Pfam: PF02345; TILa; 5.  
DR SMART: SM00181; EGF; 1.  
DR SMART: SM00137; MAM; 1.  
DR SMART: SM00214; WVC; 2.  
DR SMART: SM00216; WVD; 4.  
DR PROSITE: PS00022; EGF\_1; 1.  
DR PROSITE: PS01186; EGF\_2; 4.

DR PROSITE: PS00740; MAM\_1; 1.  
DR PROSITE: PS00600; MAM\_2; 2.  
KW Signal; Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion;  
KW Repeat.  
FT SIGNAL 1 29  
FT CHAIN 30 2476  
FT DOMAIN 30 2418  
FT TRANSMEM 2419 2439  
FT DOMAIN 2440 2476  
FT DOMAIN 31 144  
FT DOMAIN 147 312  
FT DOMAIN 319 687  
FT DOMAIN 688 799  
FT DOMAIN 800 1184  
FT DOMAIN 1185 1573  
FT DOMAIN 1574 1968  
FT DOMAIN 1969 2370  
FT DOMAIN 2366 2402  
FT DISULFID 2370 2381  
FT DISULFID 2375 2390  
FT DISULFID 2392 2401  
FT CARBOHYD 109 109  
FT CARBOHYD 269 269  
FT CARBOHYD 735 735  
FT CARBOHYD 758 758  
FT CARBOHYD 833 833  
FT CARBOHYD 1154 1154  
FT CARBOHYD 1329 1329  
FT CARBOHYD 1448 1448  
FT CARBOHYD 1544 1544  
FT CARBOHYD 1596 1596  
FT CARBOHYD 1654 1654  
FT CARBOHYD 1843 1843  
FT CARBOHYD 1965 1965  
FT CARBOHYD 2122 2122  
FT CARBOHYD 2165 2165  
FT CARBOHYD 2178 2178  
FT CARBOHYD 2329 2329  
FT CARBOHYD 2359 2359  
FT CARBOHYD 823 823  
FT CONFLICT 923 923  
FT CONFLICT 965 965  
FT CONFLICT 1241 1241  
SQ SEQUENCE 2476 AA; 270364 MW; A13B690375A6548C CRC64;  
Query Match Best Local Similarity 30.6%; Score 83.5; DB 1; Length 2476;  
Matches 26; Conservative 12; Mismatches 32; Indels 15; Gaps 3;  
OY 144 PCIGACQNFSCLE-----VQC-----PSSSTLLPFRSIALENLEPPRRQLLL 193  
DB 2369 PCLQNPCCNDGRCRGRGTHFCCECLGYGDLCT-----EPRGVSPKPPASNRVAILL 2423  
OY 194 LLLPLPLTLVLAAMGLRORARR 218  
DB 2424 GMLMPTVLIVPAVTVSKRRRRRR 2448  
RESULT 10  
LEUK\_RAT  
ID LEUK\_RAT STANDARD: PRT: 378 AA.  
AC P13838;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Leukostalin precursor (Leucocyte sialoglycoprotein) (Stalophorin)  
DE (CD43) (W3/13 antigen) (Fragment).  
GN SPN.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxId=10116;

```

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymocytes;
RX MEDLINE=816646; PubMed=2965006;
RA Killen N., Barclay A.N., Willis A.C., Williams A.F.;
RT "The sequence of rat leukostallin (w3/13 antigen) reveals a molecule
RT with O-linked glycosylation of one third of its extracellular amino
RT acids."
RL EMO J. 6:4029-4034(1987).
CC -1- FUNCTION: ONE OF THE MAJOR GLYCOPROTEINS OF THYMOCYTES AND T
CC LYMPHOCYTES. PLAYS A ROLE IN THE PHYSICO-CHEMICAL PROPERTIES OF
CC THE T-CELL SURFACE AND IN LECTIN BINDING. PRESENTS CARBOHYDRATE
CC LIGANDS TO SELECTINS. HAS AN EXTENDED RODLIKE STRUCTURE THAT COULD
CC PROTRUDE ABOVE THE GLYCOALYX OF THE CELL AND ALLOW MULTIPLE
CC GLYCAN CHAINS TO BE ACCESSIBLE FOR BINDING.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: CELL SURFACE OF THYMOCYTES, T LYMPHOCYTES,
CC NEUTROPHILS, PLASMA CELLS AND MYELOMAS.
CC -1- PTM: HAS A HIGH CONTENT OF SIALIC ACID AND O-LINKED CARBOHYDRATE
CC STRUCTURES.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y00090; CA68281.1;
DR PIR; S00842; S00842.
KW Glycoprotein; Transmembrane; Signal; T-cell; Antigen.
FT NON_TER 1 7
FT SIGNAL 1 7
FT CHAIN 8 378
FT DOMAIN 8 231
FT TRANSMEM 232 254
FT DOMAIN 255 378
FT CARBOHYD 13 13
FT CARBOHYD 15 15
FT CARBOHYD 20 20
FT CARBOHYD 23 23
FT CARBOHYD 25 25
FT CARBOHYD 27 27
FT CARBOHYD 28 28
FT CARBOHYD 29 29
FT CARBOHYD 33 33
FT CARBOHYD 34 34
FT CARBOHYD 36 36
FT CARBOHYD 37 37
FT CARBOHYD 40 40
FT CARBOHYD 108 108
FT CARBOHYD 113 113
FT CARBOHYD 118 118
FT CARBOHYD 120 120
FT CARBOHYD 124 124
FT CARBOHYD 125 125
FT CARBOHYD 126 126
FT CARBOHYD 174 174
FT CARBOHYD 176 176
FT CARBOHYD 180 180
FT CARBOHYD 183 183
FT CARBOHYD 187 187
FT CARBOHYD 189 189
SQ SEQUENCE 378 AA; 38425 MM; 231C80E8A8A257C CRC64;

Query Match 6.7%; Score 82.5; DB 1; Length 378;
Best Local Similarity 22.2%; Pred. No. 4.9;
Matches 56; Conservative 24; Mismatches 81; Indels 91; Gaps 10;
Oy 9 SPNSLLILLILLISPLCLGTPDC--YFSHSPISSNFKVKKRELT----- 50
Db 59 APASSIPL-----GTEPLSSFFFTTSAGASGNTPVP--ELTTSQEVSTEASLVLP 106

```

```

Oy 51 --DHLKIDPYTVAVNLODEKCKALMSLFLAQRMIEQLKTVAGSKMOTLLEDVNTIEHF 108
Db 107 KSSGVADEPPVIT-----NPATSSAAVASTLEFFKGTSAAPV----- 145
Oy 109 VYSCTFQPLPELARFVQTNIS-----HLKIDCTOLLAKPCIG 147
Db 146 VTSSMTSGP-----FVAITVSSETSGPVYMATGSLGPKETHTLSATIANSSGESSVA 201
Oy 148 KACQNSRCLLEVQCPDSTLLPPRSPIALEATELPEPRPOLLLILLPLTVLLAA 207
Db 202 GSTPVEFTKISTSPNPNTITVPPR-----PGSSGMLLVSMILATVTVLVVA 249
Oy 208 WCLRW-QPARR 218
Db 250 LLLMROROKRR 261

RESULT 11
APA4_MOUSE
ID APA4_MOUSE STANDARD; PRT; 395 AA.
AC P06728;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Apolipoprotein A-IV precursor (Apo-AIV).
GN APOA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=67089722; PubMed=3796595;
RA Williams S.C., Bruckheimer S.M., Lusis A.J., Leboeuf R.C.,
RA Kinlburgh A.J.;
RT "Mouse apolipoprotein A-IV gene: nucleotide sequence and induction by
RT a high-lipid diet";
RL Mol. Cell. Biol. 6:3807-3814(1986).
RN [2]
RP REVISIONS.
RA Kinlburgh A.J.;
RL submitted (DEC-1986) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; and 129/J;
RX MEDLINE=91286309; PubMed=1648102;
RA Reue K., Leete T.H.;
RT "Genetic variation in mouse apolipoprotein A-IV due to insertion and
RT deletion in a region of tandem repeats.";
RL J. Biol. Chem. 266:12715-12721(1991).
CC -1- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
CC CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
CC LIPIASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
CC COMPONENT OF HDL AND CHYLOMICRONS.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: SECRETED IN PLASMA.
CC -1- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
CC 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-
CC MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
CC HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
CC THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECTITHIN:CHOLESTEROL
CC ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
CC -1- POLYMORPHISM: THERE IS A POLYMORPHISM WITHIN A SERIES OF IMPERFECT
CC REPEATS ENCODING THE SEQUENCE E-Q-[AV]-Q. INSERTIONS OR DELETIONS
CC OF 12 NUCLEOTIDES HAVE GIVEN RISE TO THREE FORMS CHARACTERIZED BY
CC THREE (129), FOUR (C57BL/6), OR FIVE (M.CASTANEUS) COPIES OF THE
CC REPEAT UNIT.
CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

```



```

DR PROSITE: PS00741; DH_1; FALSE_NEG.
DR PROSITE: PS0010; DH_2; 1.
KM Hypothetical protein
FT DOMAIN 230 428
SQ SEQUENCE 1101 AA; 126537 MW; B26C47589676F50B CRC64;

Query Match 6.5%; Score 79; DB 1; Length 1101;
Best Local Similarity 20.0%; Pred. No. 33;
Matches 42; Conservative 32; Mismatches 66; Indels 70; Gaps 8.

QY 37 PLSNPKVKKRELETDHLKD-----PYPAVNLQDEKHKAL---WSLFLAQRW 83
|:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 815 PLSKKEKIEBDELDYMLNLFKETFNEELLSHYPPNI-YATPFKYLSSTINKKFVLLSSSP 873

QY 84 IEOLKTVAGSKMOTLIEDVN-----TEIHEVYSCFQDLPCECFEYVOTNISHLKDTCTQ 138
|:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 874 IQQLNTV-----ENLNLSENFSTDAVYHLKILQDLPESSLUKILENFISTASD---- 920

QY 139 LLLKFCIGKAGQCNFSRCLEVCQCPDS-----STLLPRSP 175
|:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 921 -LLRLRLPLKQCCPFVYKQALAIAPLSPGMSNAVELYYLAVHSRLFGTVEELPTVPSPA 979

QY 176 -----ALEATELEPEPPROL 191
Db 980 NSNNQKQDESKFQAIAMKEMPERIPKELL 1009

RESULT 14
YMW2_MYCTU
ID YMW2_MYCTU STANDARD: PRT; 122 AA.
AC OS05691;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein RV2272.
DE GN RV2272 OR MT2333 OR MTCY339.38C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RX MEDLINE=98293987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagers K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Stulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN RN
RN SEQUENCE FROM N.A.
RP RP
RC STRAIN=CDC 1551 / Oshkosh;
RA Fietischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Debay R., Dodson R., Gwyn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Uitterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT RT
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: TO E.COLI YIIB.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC

```

```
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement. (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL: Z77163; CAB00963.1; -.
DR EMBL: AE007076; AAK46616.1; -.
DR TIGR: MT2333; -.
DR Tuberculin: Ry2272; -.
DR InterPro: IPR003807; DUF202.
DR Pfam: PF02656; DUF202; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 33 53 POTENTIAL.
FT TRANSMEM 58 78 POTENTIAL.
FT TRANSMEM 97 117 POTENTIAL.
SQ SEQUENCE 122 AA; 12994 MW; 23A53754264887A7 CRC64;

Query Match 6.4%; Score 78.5; DB 1; Length 122;
Best local Similarity 33.0%; Pred. No. 3.1;
Matches 29; Conservative 12; Mismatches 24; Indels 23; Gaps 5;

QY 162 QDP-STLPPRSPALAEAT-----ELPEPRRQILLILLPLTLVLL 204
DB 13 EPDYRETLNERFTFLMORTALGLAAVALVOLVPELTIPGARQVLGVLAI---LAIL 69
QY 205 AAAMG-LRMORARRRRELHPGVLPSPHP 231
DB 70 TSGMGLRMQADRAMRRH--LPSPHP 95

RESULT 15
RCQ4 HUMAN STANDARD; PRT; 1208 AA.
MC 094761;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP-dependent DNA helicase Q4 (RecQ protein-like 4).
GN RECQ4 OR RECQ4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RX MEDLINE=90907344; PubMed=9878247;
RA Kito S., Ohsugi I., Ichikawa K., Goto M., Furuchi Y., Shimamoto A.;
RT "Cloning of two new human helicase genes of the RecQ family:
RT biological significance of multiple species in higher eukaryotes.";
RL Genomics 54:443-452(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20021764; PubMed=10552928;
RA Kito S., Lindor N.M., Shiratori M., Furuchi Y., Shimamoto A.;
RT "Rothmund-Thomson syndrome responsible gene, RECQ4: genomic structure
RT and products.";
RL Genomics 61:268-276(1999).
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- DISEASE: DEFECTS IN RECQ4 ARE A CAUSE OF ROTHMUND-THOMSON
CC SYNDROME (RTS). A DISEASE CHARACTERIZED BY DERMATOLOGICAL FEATURES
CC SUCH AS ATROPHY, PIGMENTATION, AND TELANGIECTASIA AND FREQUENTLY
CC ACCOMPANIED BY JUVENILE CATARACT, SADDLE NOSE, CONGENITAL BONE
CC DEFECTS, DISTURBANCES OF HAIR GROWTH, AND HYPOGONADISM.
CC -1- SIMILARITY: BELONGS TO THE HELICASE FAMILY. RECQ SUBFAMILY.
CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chromancer/Genes/RECQ4ID285.html".
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
```

```
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB006532; BAA74453.1; -.
DR EMBL: AB026546; BAA86899.1; -.
DR Genew: HGNC:9949; RECQ4.
DR MIM: 603780; -.
DR MIM: 268400; -.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR004589; RecQ.
DR InterPro: IPR001878; ZnF_CCHC.
DR Pfam: PF00271; DEAD_1.
DR Pfam: PF00271; Helicase_C_1.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELIC; 1.
DR SMART: SM00343; ZnF_C2HC; 1.
DR TIGRFAMs: TIGR00614; recq; 1.
KW Hydrolyase; Helicase; ATP-binding; Nuclear protein.
FT NP_BIND 502 509 ATP (POTENTIAL).
FT SITE 605 608 DEAD BOX.
SQ SEQUENCE 1208 AA; 133076 MW; CB809A7765AB48A1 CRC64;

Query Match 6.4%; Score 78.5; DB 1; Length 1208;
Best local Similarity 22.8%; Pred. No. 41;
Matches 66; Conservative 27; Mismatches 111; Indels 85; Gaps 13;

QY 9 SPNSLTL-LILLSPCLRGTPDCYS---HSPIS---SNFKVKPRELTHLKDYPV 59
DB 523 SPCLTLVSPPLSLMDQVSGLPCLAKACIHSGMTKGRSVLQKTRAQVHYLMITPE 582
QY 60 T-----VAVNIQDERHCKALMSLFLAQRWIEQLKV----- 90
DB 583 ALVAGAGLPAAQLPVAFAFACIDEAHCLISQWSHNPFCYLRCVKLBERMGVHCFGLTA 642
QY 91 -----AGSKMOTLEDVNTETIHFTVSTFQPLPECLRFVQNTNSHL---KDTCTQLL 140
DB 643 TATRRATADVAQHIAVAEEDPLH-----GPAP-----VPTN-HLTSVMDRTDQALL 689
QY 141 ALKPCIGKACQNFs-----RCLEVOCQPPSSTLLPPRSPALAEAT 180
DB 690 TLLQ--GKRPQNDLSIIYICRRREDTERIALLTCLHAAMVPPSGGRAKTTAEATYHAG 747
QY 181 ELPEPRRQILLILLPLLVLLAAAMGLRMORARRRRELHPGVLPSPHP 229
DB 748 MCSRRR-RRVQRAFMQGLRVVAVTAVFAGMGLDRPDYRAVLHLGLP-PS 794

Search completed: November 24, 2002, 10:10:43
Job time : 12.427 secs
```



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 24, 2002, 10:08:21 ; Search time 25.7766 Seconds  
(without alignments)  
1846.499 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223  
Sequence: 1 MTVALPAMSPNSLLILL...WQARRRCELHPGVLPSPHP 231

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: SP archaea:\*
- 2: SP bacteria:\*
- 3: SP fungi:\*
- 4: SP human:\*
- 5: SP invertebrate:\*
- 6: SP mammal:\*
- 7: SP mhc:\*
- 8: SP organelle:\*
- 9: SP phage:\*
- 10: SP plant:\*
- 11: SP rodent:\*
- 12: SP virus:\*
- 13: SP vertebrate:\*
- 14: SP unclassified:\*
- 15: SP viirus:\*
- 16: SP bacteriaph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	879	71.9	172	11 061104	061104 mus musculus
2	842.5	68.9	169	11 08VCH4	08VCH4 mus musculus
3	779.5	63.7	292	6 09KEX0	09KEX0 bos taurus
4	774.5	63.3	292	6 08BNW1	08BNW1 bos taurus
5	774	63.3	294	6 09MZV0	09MZV0 canis fam11
6	761	62.2	291	6 09MKD9	09MKD9 felis silve
7	678.5	55.5	274	6 09GKDP	09GKDP bos taurus
8	95.5	7.8	909	10 042484	042484 arabidopsis
9	94	7.7	355	4 09H665	09H665 homo sapien
10	93.5	7.6	510	6 09BGT6	09BGT6 macaca fasc
11	90.5	7.4	909	10 09ASPS	09ASPS arabidopsis
12	88.5	7.2	326	12 083443	083443 murine rota
13	88.5	7.2	326	12 083448	083448 murine rota
14	88	7.2	258	4 09H563	09H563 homo sapien
15	88	7.2	765	4 094824	094824 homo sapien
16	88	7.2	843	4 014584	014584 homo sapien

17	88	7.2	1028	5 08SXA6	08SXA6 drosophila
18	88	7.2	1254	5 09VF51	09VF51 drosophila
19	87.5	7.2	477	11 09CYB2	09CYB2 mus musculus
20	87.5	7.2	1231	10 09FKE2	09FKE2 arabidopsis
21	87	7.1	291	16 08ZAH9	08ZAH9 yersinia pe
22	87	7.1	1256	5 09VF50	09VF50 drosophila
23	86.5	7.1	2111	5 091802	091802 drosophila
24	86.5	7.1	4167	5 09GPN8	09GPN8 drosophila
25	86	7.0	962	5 096164	096164 plasmodium
26	85	7.0	181	5 017726	017726 caenorhabd1
27	85	7.0	1305	2 006521	006521 enterococcu
28	85	7.0	4513	10 09MBF8	09MBF8 chlamydomon
29	84.5	6.9	364	4 096AY5	096AY5 homo sapien
30	84.5	6.9	939	16 09KOC8	09KOC8 vibrio chol
31	84	6.9	330	5 09N4U7	09N4U7 caenorhabd1
32	83.5	6.8	588	8 09B6D1	09B6D1 yarrowia li
33	83	6.8	258	4 09UMT2	09UMT2 homo sapien
34	83	6.8	267	5 09W2D7	09W2D7 drosophila
35	83	6.8	341	5 08T0N4	08T0N4 drosophila
36	83	6.8	1059	5 09VNP5	09VNP5 drosophila
37	82.5	6.7	326	12 085032	085032 porcine rot
38	82.5	6.7	326	12 085034	085034 porcine rot
39	82.5	6.7	335	8 09ZYX32	09ZYX32 orycteropu
40	82.5	6.7	379	8 09T7T9	09T7T9 tapirus ind
41	82.5	6.7	431	10 09SN38	09SN38 arabidopsis
42	82.5	6.7	809	11 09DBY4	09DBY4 mus musculu
43	82.5	6.7	1266	10 09XET3	09XET3 lycopersico
44	82	6.7	575	10 09LS68	09LS68 arabidopsis
45	81.5	6.7	659	4 09H9U7	09H9U7 homo sapien

ALIGNMENTS

RESULT 1

ID	061104	PRELIMINARY:	PRT:	172 AA.
AC	061104:			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Flt3 ligand, T169 form.			
GN	FLT3L.			
OS	Mus musculus (Mouse).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	McClanahan T., Culpepper J., Campbell D., Wagner J., Franz-Bacon K.,			
RA	Mattson J., Tsai S., Luh J., Guimares M.J., Mattel M.-G., Rosnet O.,			
RA	Birnbaum D., Hannum C.;			
RT	"Flt3 ligand: expression, genomic organization, alternatively spliced			
RT	forms and processing."			
RL	Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; U44024; AAA93305.1; -			
DR	MGI: 95560; FLT3L.			
DR	InterPro: IPR004213; Flt3_lig.			
DR	InterPro: IPR001230; Prenyl_site.			
DR	Pfam: PF02947; Flt3_lig.1.			
DR	PROSITE: PS00294; PRENYLATION; UNKNOWN.1.			
SO	SEQUENCE 172 AA; 19465 MW; 04FOA01017E3384 CRC64;			

Query Match 71.9% Score 879; DB 11; Length 172;

Best Local Similarity 98.2%; Pred. No. 1.5e-81; Mismatches 2; Indels 0; Gaps 0;

QY	1	MTVALPAMSPNSLLILLSPCLRGTPDCYFSHSPSSNFYKFKRELTDHLKDPVT	60
DB	1	MTVALPAMSPNSLLILLSPCLRGTPDCYFSHSPSSNFYKFKRELTDHLKDPVT	60
OY	61	VAVNLDKCKALMSLFLAQRWIEOLKTYAGSKMOTLLEDVTEHFVNSCPQPLPEC	120

```

Db 61 VAVNLQDEKHKALMSFLAQRWIEOLKTAVAGSKMOTLLEVDNTEIHFTVTSCTFOPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDPSSTL 168
    |||||||
Db 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDPSVSL 168

RESULT 2
Q8VCH4 PRELIMINARY; PRT; 169 AA.
AC Q8VCH4;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Similar to FMS-like tyrosine kinase 3 ligand.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RA Strausberg R.;
RL EMBL; BC019801; A019801.1; -
DR InterPro: IPR004213; Flt3_lig.
DR Pfam: PF02947; flt3_lig; 1.
KW KINASE.
SQ SEQUENCE 169 AA; 18986 MW; 5B4CA7D9724EEF2 CRC64;

Query Match 68.9%; Score 842.5; DB 11; Length 169;
Best Local Similarity 92.5%; Pred. No. 7.7e-78;
Matches 161; Conservative 0; Mismatches 4; Indels 9; Gaps 1;

QY 1 MTVLAPAMSPNSLLILLISPCIRGTGPDYFSPSHSPSSNFVKYKRELTDHLKDYPT 60
Db 1 MTVLAPAMSPNSLLILLISPCIRGTGPDYFSPSHSPSSNFVKYKRELTDHLKDYPT 60
QY 61 VAVNLQDEKHKALMSFLAQRWIEOLKTAVAGSKMOTLLEVDNTEIHFTVTSCTFOPLPEC 120
    |||||||
Db 61 VAVNLQDEKHKALMSFLAQRWIEOLKTAVAGSKMOTLLEVDNTEIHFTVTSCTFOPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDPSSTLPPRSP 174
    |||||||
Db 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDPSSTLPPRSP 174

RESULT 3
Q8GKEO PRELIMINARY; PRT; 292 AA.
AC Q8GKEO;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Flt3 ligand isoform-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20570936; PubMed=11120823;
RA Wang J., Brown W.C., Palmer G.H.;
RT Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain
RT required for receptor binding and function using naturally occurring
RT ligand isoforms.
RL J. Immunol. 165:6966-6974(2000).
DR EMBL; AF282985; AAF93322.1; -
DR InterPro: IPR004213; Flt3_lig.
DR Pfam: PF02947; flt3_lig; 1.
SQ SEQUENCE 292 AA; 32390 MW; D66B9ED79221202D CRC64;

```

```

Query Match 63.7%; Score 779.5; DB 6; Length 292;
Best Local Similarity 63.2%; Pred. No. 3.7e-71;
Matches 165; Conservative 20; Mismatches 43; Indels 33; Gaps 5;

QY 1 MTVLAPAMSPNSLLILLISPCIRGTGPDYFSPSHSPSSNFVKYKRELTDHLKDYPT 60
    |||||||
Db 1 MTVLAPAMSPNSLLILLISPCIRGTGPDYFSPSHSPSSNFVKYKRELTDHLKDYPT 60
QY 61 VAVNLQDEKHKALMSFLAQRWIEOLKTAVAGSKMOTLLEVDNTEIHFTVTSCTFOPLPEC 120
    |||||||
Db 61 VAVNLQDEKHKALMSFLAQRWIEOLKTAVAGSKMOTLLEVDNTEIHFTVTSCTFOPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDPSSTLPPRSP 180
    |||||||
Db 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDPSSTLPPRSP 180
QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDPSSTLPPRSP 180
    |||||||
Db 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDPSSTLPPRSP 180
QY 181 ELPEPR-PROILLILLPLTVLLAAAGL-RWQARR- 218
    |||||||
Db 179 SLPGQSPILLILLPLTVLLAAAGL-RWQARR- 218
    |||||||
QY 219 -----GELHPGVLPSPHP 231
    |||||||
Db 239 DTESLGGSQLPFG-PFLGHP 258

RESULT 4
Q8NMNL PRELIMINARY; PRT; 292 AA.
AC Q8NMNL;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Flt3 ligand.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Hikono H., Komotani E.;
RT Cloning of a cDNA for bovine flt3 ligand.
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051841; BAB79634.1; -
DR InterPro: IPR004213; Flt3_lig.
DR Pfam: PF02947; flt3_lig; 1.
SQ SEQUENCE 292 AA; 32388 MW; 2A797EC1199C1D9 CRC64;

Query Match 63.3%; Score 774.5; DB 6; Length 292;
Best Local Similarity 62.8%; Pred. No. 1.2e-70;
Matches 164; Conservative 20; Mismatches 44; Indels 33; Gaps 5;

QY 1 MTVLAPAMSPNSLLILLISPCIRGTGPDYFSPSHSPSSNFVKYKRELTDHLKDYPT 60
    |||||||
Db 1 MTVLAPAMSPNSLLILLISPCIRGTGPDYFSPSHSPSSNFVKYKRELTDHLKDYPT 60
QY 61 VAVNLQDEKHKALMSFLAQRWIEOLKTAVAGSKMOTLLEVDNTEIHFTVTSCTFOPLPEC 120
    |||||||
Db 61 VAVNLQDEKHKALMSFLAQRWIEOLKTAVAGSKMOTLLEVDNTEIHFTVTSCTFOPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDPSSTLPPRSP 180
    |||||||
Db 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDPSSTLPPRSP 180
QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDPSSTLPPRSP 180
    |||||||
Db 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDPSSTLPPRSP 180
QY 181 ELPEPR-PROILLILLPLTVLLAAAGL-RWQARR- 218
    |||||||
Db 179 SLPGQSPILLILLPLTVLLAAAGL-RWQARR- 218
    |||||||
QY 219 -----GELHPGVLPSPHP 231
    |||||||
Db 239 DTESLGGSQLPFG-PFLGHP 258

```



## RESULT 5

Q9MZV0 PRELIMINARY: PRT: 294 AA.

AC Q9MZV0; 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Flt3 ligand.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI\_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20358731; PubMed=10902925;

RA Yang S., Sim G.K.;

RT "Molecular cloning of canine and feline flt3 ligand reveals high

RT degree of similarity to the human and mouse homologue but uniquely

RT long cytoplasmic domain."

RL DNA Seq. 11:163-166(2000).

DR EMBL; AF155148; AAF87088.1; -.

DR InterPro: IPR004213; Flt3\_1lg.

DR Pfam: PF02947; flt3\_1lg. 1.

SQ SEQUENCE 294 AA; 32394 MW; 6859917AB74ABCD CRC64;

Query Match 63.3%; Score 774; DB 6; Length 294;

Best Local Similarity 70.2%; Pred. No. 1.3e-70;

Matches 158; Conservative 23; Mismatches 38; Indels 6; Gaps 4;

QY 1 MYVLAPAMSPNSLLLLLSPLCRGTGTCYFSHSPISSNFVKFRELTDHLKDPVT 60

DB 1 MYVLAPAMSPRTS-LLLLLLSPLGKGTGTCFSHSPISTFAVITRKLSLDYLDYPT 59

QY 61 VAVNLDEKHCKALMSFLAQRWIEQLKTVAGSKMOTLEDVNTLHFVTSCTFOPLEPC 120

DB 60 VASNLDDDELGCAGFWRLVLAQRWWRQLQVAGSQMILLEAVNTEHFVTFCAFQPLPSC 119

QY 121 LRFVQTNISHLKTCYQLALAKPCIGKACONFSRCLEVOQCPDSTLLPPSPALAEAT 180

DB 120 LRFVQTNISHLQDTSQALAKLPWTR--RNFSGCLLEQCPDSTLVPSPALAEAT 177

QY 181 ELPEPR-PROLLLLLLPLTLVLAAMGLRMORARRRGEIHPG 224

DB 178 ALPAPQAPR-LLLLLLPVALLLMSTAMCLHMRRRRRRRSPYPG 220

RESULT 6

Q9MZU9 PRELIMINARY: PRT: 291 AA.

AC Q9MZU9; 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Flt3 ligand.

OS Fells silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

OX NCBI\_TaxID=9685;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20358731; PubMed=10902925;

RA Yang S., Sim G.K.;

RT "Molecular cloning of canine and feline flt3 ligand reveals high

RT degree of similarity to the human and mouse homologue but uniquely

RT long cytoplasmic domain."

RL DNA Seq. 11:163-166(2000).

DR EMBL; AF155149; AAF87089.1; -.

DR InterPro: IPR004213; Flt3\_1lg.

DR Pfam: PF02947; flt3\_1lg. 1.

SQ SEQUENCE 291 AA; 32459 MW; 8F85A10A5EA0DCC6 CRC64;

Query Match 62.2%; Score 761; DB 6; Length 291;

Best Local Similarity 71.1%; Pred. No. 2.8e-69;

Matches 155; Conservative 22; Mismatches 37; Indels 4; Gaps 3;

QY 1 MYVLAPAMSPNSLLLLLSPLCRGTPCPCYFSHSPISSNFVKFRELTDHLKDPVT 60

DB 1 MYVLAPAMSPRTS-LLLLLLSPLGRSPDCSFHSPISTFAVITRKLSLDYLDYPT 59

QY 61 VAVNLDEKHCKALMSFLAQRWIEQLKTVAGSKMOTLEDVNTLHFVTSCTFOPLEPC 120

DB 60 VASNLDDDELGCAGFWRLVLAQRWWRQLQVAGSQMILLEAVNTEHFVTFCAFQPLPSC 119

QY 121 LRFVQTNISHLKTCYQLALAKPCIGKACONFSRCLEVOQCPDSTLLPPSPALAEAT 180

DB 120 LRFVQTNISHLQDTSEQLALKPWTR--RNFSGCLLEQCPDSTLVPSPALAEAT 177

QY 181 ELPEPR-PROLLLLLLPLTLVLAAMGLRMORARRR 218

DB 178 ALPAPQAPR-LLLLLLPVALLLMSAAMCLHMRRRRR 214

RESULT 7

Q9GKD9 PRELIMINARY: PRT: 274 AA.

AC Q9GKD9; 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Flt3 ligand isoform-2.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;

OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20570936; PubMed=11120823;

RA Mwangi W., Brown W.C., Palmer G.H.;

RT "Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain

RT required for receptor binding and function using naturally occurring

RT ligand isoforms."

RL J. Immunol. 165:6966-6974(2000).

DR EMBL; AF282986; AAF9323.1; -.

DR InterPro: IPR004213; Flt3\_1lg.

DR Pfam: PF02947; flt3\_1lg. 1.

SQ SEQUENCE 274 AA; 30372 MW; 725A7F7A95DA98B CRC64;

Query Match 55.5%; Score 678.5; DB 6; Length 274;

Best Local Similarity 57.3%; Pred. No. 6.4e-61;

Matches 150; Conservative 19; Mismatches 41; Indels 51; Gaps 6;

QY 1 MYVLAPAMSPNSLLLLLSPLCRGTPCPCYFSHSPISSNFVKFRELTDHLKDPVT 60

DB 1 MYVLAPAMSPRTSLLLLLSPLGQSTPCSFHSPISTFAIKIGLSKYLLODPVT 60

QY 61 VAVNLDEKHCKALMSFLAQRWIEQLKTVAGSKMOTLEDVNTLHFVTSCTFOPLEPC 120

DB 61 VASNLDDDELGCAGFWRLVLAQRWWRQLQVAGSEKLELDVNTLHFVTSCTFOPLEPC 115

QY 121 LRFVQTNISHLKTCYQLALAKPCIGKACONFSRCLEVOQCPDSTLLPPSPALAEAT 180

DB 120 LRFVQTNISHLQDTSEQLALKPWTR--RNFSGCLLEQCPDSTLVPSPALAEAT 177

QY 181 ELPEPR-PROLLLLLLPLTLVLAAMGLRMORARRR 218

DB 178 ALPAPQAPR-LLLLLLPVALLLMSAAMCLHMRRRRR 214

RESULT 8

Q42484

```

ID      0042484: PRELIMINARY; PRT; 909 AA.
AC
DT      01-NOV-1996 (TRMBLrel. 01, Created)
DT      01-NOV-1996 (TRMBLrel. 01, Last sequence update)
DT      01-JUN-2002 (TRMBLrel. 01, Last annotation update)
DE      RPS2 (Disease resistance protein RPS2).
DE      RPS2 OR F20B18.200 OR At4G626090.
GN      Arabidopsis thaliana (Mouse-ear cress).
OS      Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC      Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae;
OC      eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX      NCBI_TaxID=3702;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=COL-0;
RX      MEDLINE=94377978; PubMed=8091210;
RA      Bent A.F., Kunkel B.N., Dahlbeck D., Brown K.L., Schmidt R.,
RA      Citraudat J., Leung J., Shalaskiewicz B.J.;
RA      "RPS2 of Arabidopsis thaliana: a leucine-rich repeat class of plant
RT      disease resistance genes."
RL      Science 265:1856-1860(1994).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=95007758; PubMed=7923358;
RA      Mindrinos M., Katagiri F., Yu G., Ausubel F.M.;
RA      "The A. thaliana disease resistance gene RPS2 encodes a protein
RT      containing a nucleotide-binding site and leucine-rich repeats."
RL      Cell 78:1089-1099(1994).
RN      [3]
RP      SEQUENCE FROM N.A.
RA      Bevan M., Rose M., Hempel S., Entian K.-D., Hohenseil J., Mewes H.W.,
RA      Mayer K.F.X., Schneller C.;
RA      Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      [4]
RP      SEQUENCE FROM N.A.
RA      EU Arabidopsis sequencing project;
RA      Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN      [5]
RP      SEQUENCE FROM N.A.
RA      Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K.,
RA      Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL      [6]
RP      SEQUENCE FROM N.A.
RA      EU Arabidopsis sequencing project;
RA      Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL      EMBL: U115158; AAA21874.1; -;
DR      EMBL: U12860; AAA50236.1; -;
DR      EMBL: AL049483; CAB39674.1; -;
DR      EMBL: AL161564; CAB39464.1; -;
DR      InterPro: IPR000767; Disease_resist.
DR      InterPro: IPR001611; LRR.
DR      InterPro: IPR002182; NB-ARC.
DR      Pfam: PF00560; LRR; 4.
DR      Pfam: PF00931; NB-ARC; 1.
DR      PRINTS: PR00364; DISEASESISIT.
SQ      SEQUENCE 909 AA; 104640 MW; D279B6E30E49D640 CRC64;

```

```

OY      149 ACONFSRCLEFYCCPDSSSTLTPRSPALATELPERPRPOLLLLLLLPLFUTVILAAAN 208
        :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      715 HGRNRR-LSTKSCHDEBYLV---TPADFEWDWLPs---LEVELHSLHNLTFRV-----W 762C
QY      209 G 209
        |
Db      763 G 763

RESULT 9
Q9H665          PRELIMINARY;           PRT;       355 AA.
AC      Q9H665;
DT      01-MAR-2001 (TREMBLrel_16, Created)
DT      01-MAR-2001 (TREMBLrel_16, last sequence update)
DT      01-DEC-2001 (TREMBLrel_19, last annotation update)
DE      CDNA: FLJ22573 f1s, clone HS102387.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX      NCBI_TaxID=9606;
        [!]
RN      SEQUENCE FROM N.A.
RP
RC      TISSB-SMALL INTERINE;
RA      Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
RA      Suzuki Y., Oobayashi M., Nishi T., Shibahara T., Tanaka T.,
RA      Nakamura Y., Isoigai T., Sugano S.;
RT      "NEDO human cDNA sequencing project.";
RL      submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL, AK026226; BABI5400.1; -.
SQ      SEQUENCE   355 AA;  37894 MW;   52C4A173E673623C CRC64;
```

	Query Match:	7.7%	Score 94;	DB 4;	Length 355;
	Best Local Similarity	20.6%;	Pred. No. 0.25;	Mismatches 41;	Conservative 15; Indels 84; Gaps 6;
QY	116 PLPE---	CLRFVQTINSHLKDTCGLALPKC-----IGKAC-----QNFSCRLL	157		
		:	:	:	
Ddb	18 PPPPAGCYCGRLRYWPNDKKCCSCLGRGPPPCDYEFRNCGLDNDHGFVPFPFKCS	77			
QY	158 EVGCCPDSSILPLP-----		171		
Ddb	78 SGCCNPBGAEELCSPCGGAVTPPTPAAGGRTFWRCRERHPVAKGCHFLTGNBAPSSOE	137			
QY	172 -RSPIDLEAFELDEPPRP-----	LILLILLPLTVLLLAAMGDPRWARRRSGE	220		
		:	:	:	
Ddb	138 RSSPASSIAMRTPEEPQQAMFNFLPYVLVLTLLAVIATILLITLIMHCWKERADPR	197			
QY	221 LHPGV-----	PLPSH 230			
	:     :				
Ddb	198 PYPGLVGVPNTHTPSSH	216			
RESULT 10					
Q9BGY6	ID	PRELIMINARY;	PRT;	510 AA.	
AC	Q9BGY6;				
DT	01-JUN-2001 (TREMBLrel. 17,	Created)			
DT	01-JUN-2001 (TREMBLrel. 17,	Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21,	Last annotation update)			
DE	Hypothetical 56.5 kDa protein.				
OS	Macaqa fascicularis (Crab eating macaque) (Cynomolgus monkey).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;				
OC	Cercopithecinae; Macaca.				
OX	NCBI_TaxID=9541;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=FRONTAL LOBE LEFT;				
RA	Ogasa N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,				
RA	Suzuki Y., Sugano S., Hashimoto K.;				
FT	"Isolation of full-length cDNA clones from macaque brain CDNA				
ET	libraries.";				

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB055271; BAB21895.1; -  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000483; LRR\_Cterm.  
 DR InterPro: IPR003592; LRR\_out.  
 DR InterPro: IPR003591; LRR\_typ.  
 DR Pfam: PF00560; LRR\_6.  
 DR Pfam: PF01463; LRRCT\_1.  
 DR PRINTS: PR00019; LEONICHRPT.  
 DR SMART: SM00370; LRR\_4.  
 DR SMART: SM00369; LRR\_typ; 6.  
 KW Hypothetical protein.  
 SO SEQUENCE 510 AA; 56496 MW; FF52698C2F9119E8 CRC64;

Query Match 7.6%; Score 93.5; DB 6; Length 510;  
 Best Local Similarity 23.9%; Pred. No. 0.43;  
 Matches 68; Conservative 34; Mismatches 105; Indels 77; Gaps 14;

QY 9 SPSSLLILLLLSPCLRTGTPD-----CYFSHSPISSNFKVKFRELTDHL- 53  
 DB 50 STSLSLLEFNLALLSLRNGIEDVDALDGLTMLTLLLEHNQISS-----SLTDHTE 103  
 QY 54 --LKDYPTVAVN-----LQDE--KHCKALMSLETLAQHWIEQL--KTVAGSKMOTL--LE 100  
 DB 104 SKLHSIQVLYVLSNNALRTLRGSMFNRTRGLTRQLDGNQITNLTDSSFGTINLSLRHLD 163  
 QY 101 DVNTEIHFVTSCTPOPLPECTLRFYQTN-----ISHLKD-----TCQQL 140  
 DB 164 LSNMFISTYIGKADFRLPG--LQEVDSRRRLAHMPDVTEPLKQLHLHSLDKNQNSCTCDL 222  
 QY 141 -----ALKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSPIALEATELPEPRROLLL- 193  
 DB 223 HPLARLRNVKISSANTLTLMNAKDLNCPSTAVAAQSVLRISFTNCDPKAPNFTLVYKD 282  
 QY 194 -LLLP-----LTIYLLAAWGL-----RMQARRRGELH 222  
 DB 283 RSPLLPGQVALLTVLGFAGAVGLTCLGLVNMKLLQGGKANEH 326

RESULT 11  
 Q9ASPS PRELIMINARY; PRT; 909 AA.  
 AC Q9ASPS;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DE Disease resistance protein RPS2.  
 OS Arabidopsis thaliana (mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2131631; PubMed=1133251;  
 RA Banerjee D., Zhang X., Bent A.F.;  
 RT "The leucine-rich repeat domain can determine effective interaction  
 between Rps2 and other host factors in Arabidopsis RPS2-mediated  
 disease resistance.";  
 RT Genetics 158:439-450(2001).  
 RL EMBL: AF368301; AAK38117.1; -  
 DR EMBL: IPR003593; AAA\_Atpase.  
 DR InterPro: IPR000767; Disease\_resist.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR003592; LRR\_out.  
 DR InterPro: IPR002182; NB-ARC.  
 DR Pfam: PF00560; LRR\_4.  
 DR Pfam: PF00931; NB-ARC; 1.  
 DR PRINTS: PR00364; DISEASERSIST.  
 DR SMART: SM00382; AAA; 1.  
 DR SMART: SM00370; LRR; 4.  
 KW ATP-binding.  
 SO SEQUENCE 909 AA; 104613 MW; FB3E0F881B409DFA CRC64;

Query Match 7.4%; Score 90.5; DB 10; Length 909;  
 Best Local Similarity 22.8%; Pred. No. 1.7;  
 Matches 55; Conservative 38; Mismatches 91; Indels 57; Gaps 11;

QY 14 LLLILLLLSPCLRTGTPDQYFSHSPISSNFKVKFRELTD-----HLKQDPVYVA----- 62  
 DB 535 LTTLMQONSYLKRTIPFPMHMPVLRVLDLSTFTSIEIPISIVLYELVHLSNGTKIS 594  
 QY 63 -----VNLQDEKHCKALMSLEL-----AQHWIEQLKV-----AGSKMOTLLEDPVT 104  
 DB 595 VLPQELGNLRKRLKHLDLQRTQELQTPRDAICNLSKLEVLNLYSVAGWGLQSPQDEVE 654  
 QY 105 ETHF-----VTSCTPQPLPECLAF--VQNIHSLKDTCTQLLALK-PTGK 148  
 DB 655 ELGFADLEYLENLTGLITVLSLETTLTFEGALHKHIQHLHVEECNDLLYFNLPSTYN 714  
 QY 149 ACQNFSCLEVOCCPDSSSTLLPPRSPIALEATELPEPRROLLLLLLPLTVLLAAW 208  
 DB 715 HGRNLR--LSISCHDLELY--TPADFENDLPS--LEVLTLHSLHNLTRV-----W 762  
 QY 209 G 209  
 DB 763 G 763

RESULT 12  
 Q83443 PRELIMINARY; PRT; 326 AA.  
 AC Q83443;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE VP7.  
 OS Murine rotavirus.  
 OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.  
 OX NCBI\_TaxID=28527;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EC;  
 RX MEDLINE=94330134; PubMed=8053149;  
 RA Dunn S.J., Burns J.W., Cross T.L., Vo P.T., Ward R.L., Brenton M.,  
 RA Greenberg H.B.; VP4 and VP7 of five murine rotavirus strains.";  
 RT "Comparison of VP4 and VP7 of five murine rotavirus strains.";  
 RL Virology 203:250-259(1994).  
 DR EMBL: U084422; AAB50485.1; -  
 DR InterPro: IPR001963; VP7.  
 DR Pfam: PF00434; VP7; 1.  
 DR ProDom: PD000191; VP7; 1.  
 SO SEQUENCE 326 AA; 36990 MW; B579E98A10DCF8A6 CRC64;

Query Match 7.2%; Score 88.5; DB 12; Length 326;  
 Best Local Similarity 30.0%; Pred. No. 0.84;  
 Matches 24; Conservative 11; Mismatches 28; Indels 17; Gaps 2;

QY 15 LLLILLLLSPCLR-----GTPDCYFSHSPISSNFKVKFRELTDHLKDYPTVA 63  
 DB 38 LVLVILLSPCITAGNNGINMLPTGSMDTAYANSTOSDIF-----LSTLCLYPTPAAT 91  
 QY 64 NLQDEKHCKALMSLETLAQHW 83  
 DB 92 EMDNDSWKDTLSQLFLTKGM 111

RESULT 13  
 Q83448 PRELIMINARY; PRT; 326 AA.  
 AC Q83448;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE VP7.  
 OS Murine rotavirus.

[illegible]

Dd	167	ESPSTIPVSPQPNSTLRGPAALVALPV-----FCGLLVASTVLSTALLVMWVL	217	
OY	211	WMQRARRRG--LHEGVPLP	228	
		: :		
Dd	218	RNRHMOHGSRSLHFHAQPRP	237	
	RESULT 15			
ID	094824	PRELIMITARY;	PRT; 765 AA.	
AC	094824;			
DT	01-MAY-1999 (TREMBLrel, 10,	Created)		
DT	01-MAY-1999 (TREMBLrel, 10,	Last sequence update)		
DE	01-MAR-2002 (TREMBLrel, 20,	Last annotation update)		
DE	KIAA0716 protein.			
GN	KIAA0716.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=BRAIN:			
KX	MEDLINE=99087487; PubMed=9872452;			
RA	Nagase T., Ishikawa K., Suyama M., Kikuno R., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;			
RT	"Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."			
RL	DNA Res. 5:277-286(1998).			
DR	EMBL: AB018259; BAA34436.1; -			
DR	InterPro: IPR000194; ATPASE_ALPHA_BETA; UNKNOWN_1			
DR	PROSITE: PS00152; ATPASE_ALPHA_BETA; UNKNOW_1			
SQ	SEQUENCE 765 AA; 86915 MW; EICCAE0771A9E9F9 CRC64;			
	Query Match	7.2%; Score 88; DB 4; Length 765;		
	Best Local Similarity	20.1%; Pred. No. 2.5;		
	Matches 51; Conservative	29; Mismatches 58; Indels 116; Gaps	14;	
OY	27	GPPDCYFSHPSSNFKVFRELTHLK---DYPTAVNVLDENHKCALW---SLEFL	79	
Dd	236	GVPD-----NIKS-YKV-----NIMVKFRDYPRHKGTK-DKENEFKSLWVERTSKYL	282	
OY	80	AQ-----RW----IEDLTVGASGMQT--LLEDVNTETI-H-EVTSC-----TFQPLECL	121	
Dd	283	VQSLPEISMSFEVEKEKEVEVEMSPLENATIVLEENKNOQLKTLLISQCOTROMONINPLYMQL	342	
OY	122	-----	-RFV	124
Dd	343	NGVTAADVNGVSROAEFFVKEYILSHPEDGEKIARLRELMLEQAQLLEFGLAHYEKTV	402	
OY	125	QFNISHLLKDTCQLDLAKPCIGKACQNSRCLLEVQ-----CQ-----PDS	165	
Dd	403	QDMRMRLHKLVDOGFVWMSLGC--IQESACMQASPAPFPNGSPVCNSAPASVSDG	460	
OY	166	STLLPSPRALAEA	179	
		: : :         :		
Dd	461	TRVTPRRSLSTPYA	474	

Search completed: November 24, 2002, 10:11:41  
Job time : 28.7768 secs

Job time : 28.7768 secs



PR 03-DEC-1993; 93US-0162407.  
 PR 07-MAR-1994; 94US-0209502.  
 PR 11-MAY-1994; 94US-0243545.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Beckmann MP, Lyman SD;  
 XX  
 DR WPI: 1995-008071/02.  
 DR N-PSDB: AA079076.  
 XX  
 PT Isolated ligands for flt3 receptors - useful for treating  
 PT anemia, AIDS and various cancers  
 XX  
 PS Disclosure; Page 25-27; 33pp; English.  
 XX  
 CC cDNA encoding mouse flt3-ligand (flt3-L) was isolated from a  
 CC cDNA library of T-cell line F7B-0.3A4 in CV-1/EBNA-1 cells  
 CC using a slide autoradiography method. Flt3-L stimulates  
 CC production of progenitor and stem cells, and can be used e.g.  
 CC in gene therapy protocols.  
 CC  
 SQ Sequence 231 AA;

Query Match 100.0%; Score 1223; DB 16; Length 231;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-115;  
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTVLAPAMSPNSLLLLLSPLCRGTGTPDCYFSPISSEFKYKRELTDHLKDYPT 60  
 DB 1 MTVLAPAMSPNSLLLLLSPLCRGTGTPDCYFSPISSEFKYKRELTDHLKDYPT 60  
 OY 61 VAVNIQDEKHKALMSLEFLAQRWIEQLKTVAAGSKMOTLLEDVNTLHFWTSCTFQPLPEC 120  
 DB 61 VAVNIQDEKHKALMSLEFLAQRWIEQLKTVAAGSKMOTLLEDVNTLHFWTSCTFQPLPEC 120  
 OY 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPIALEAT 180  
 DB 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPIALEAT 180  
 OY 181 ELPEPRRQQLLLLLLPLTLVLLAAWGLRMQARRRGELHPGVPLPSHP 231  
 DB 181 ELPEPRRQQLLLLLLPLTLVLLAAWGLRMQARRRGELHPGVPLPSHP 231

# RESULT 2

AAW67768  
 ID AAW67768 standard; Protein; 231 AA.

XX AC AAW67768;  
 XX  
 DT 25-MAR-1999 (first entry)  
 XX  
 DE Murine flt3-ligand.  
 XX  
 KW Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L;  
 KW immunogenic; autoimmune disease; organ transplantation; food allergy;  
 XX tissue transplantation.  
 XX  
 OS Mus sp.  
 XX  
 PN MO9857655-A1.  
 XX  
 PD 23-DEC-1998.  
 XX  
 PF 12-JUN-1998; 98MO-US12085.  
 XX  
 PR 17-JUN-1997; 97US-0877421.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Abbott NM, Mowat AM, Viney JL;  
 XX

DR WPI: 1999-070422/06.  
 DR N-PSDB: AAW81505.

PT Methods for initiating or enhancing antigen specific immune  
 PT tolerance - by using murine or human flt3 ligand  
 XX  
 PS Claim 1; Page 12; 25pp; English.  
 XX

CC A method has been developed of initiating or enhancing: (i) an antigen-  
 CC specific immune tolerance; or (ii) immunotolerance of a therapeutic  
 CC immunogenic molecule by addition of a polypeptide, before, after or with  
 CC the mucosal administration of an immunotolerising amount of the antigen  
 CC or therapeutic molecule, respectively. The polypeptide is capable of  
 CC binding the flt3 receptor and is: a) amino acids 28-x of murine flt3  
 CC ligand (flt3-L), where x is an amino acid between 163-231; b) amino  
 CC acids 28-y of human flt3-L, where y is an amino acid between 160-235;  
 CC and c) a polypeptide that has at least 90% identity to the polypeptides  
 CC of either (a) or (b). The method ameliorates the effects of autoimmune  
 CC diseases, food allergies or organ or tissue rejection following  
 CC transplantation. Administration of flt3-L allows lower doses of antigens  
 CC to be used in vivo for mucosally administered antigens. The present  
 CC sequence represents murine flt3-L.  
 CC  
 SQ Sequence 231 AA;

Query Match 100.0%; Score 1223; DB 20; Length 231;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-115;  
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTVLAPAMSPNSLLLLLSPLCRGTGTPDCYFSPISSEFKYKRELTDHLKDYPT 60  
 DB 1 MTVLAPAMSPNSLLLLLSPLCRGTGTPDCYFSPISSEFKYKRELTDHLKDYPT 60  
 OY 61 VAVNIQDEKHKALMSLEFLAQRWIEQLKTVAAGSKMOTLLEDVNTLHFWTSCTFQPLPEC 120  
 DB 61 VAVNIQDEKHKALMSLEFLAQRWIEQLKTVAAGSKMOTLLEDVNTLHFWTSCTFQPLPEC 120  
 OY 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPIALEAT 180  
 DB 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPIALEAT 180  
 OY 181 ELPEPRRQQLLLLLLPLTLVLLAAWGLRMQARRRGELHPGVPLPSHP 231  
 DB 181 ELPEPRRQQLLLLLLPLTLVLLAAWGLRMQARRRGELHPGVPLPSHP 231

# RESULT 3

AAW20186  
 ID AAW20186 standard; Protein; 231 AA.

XX AC AAW20186;  
 XX  
 DT 14-MAY-2001 (first entry)  
 XX  
 DE Mouse Flt-3 ligand.  
 XX  
 KW Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;  
 KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;  
 KW lymphoma; autoimmune disease; infection; gene therapy.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key  
 FH Peptide 1..27  
 FT /label= Signal\_peptide  
 FT 28..231  
 FT /label= Mature\_protein  
 FT 28..188  
 FT /label= Extracellular\_domain  
 FT 189..211  
 FT /label= Transmembrane\_domain  
 FT 212..231  
 FT /label= Cytoplasmic\_domain

XX XX WO200109303-A2.  
XX PN 08-FEB-2001.  
XX PD  
XX PF 31-JUL-2000; 2000MO-US20679.  
XX PR 30-JUL-1999; 990S-0146170.  
XX PA (VICA-) VICAL INC.  
XX PI Hermanson GG;  
XX XX  
XX DR WPI; 2001-123319/13.  
XX DR N-PSDB; AAF30305.  
XX PT Immunogenic compositions comprising Flt-3 ligand encoding  
XX PT polynucleotides and one or more antigen, or cytokine encoding  
XX PT autoimmune diseases (e.g. rheumatoid arthritis) -  
PS Claim 2; Page 120; 149pp; English.  
XX XX  
CC The present sequence is that of mouse Fms-like tyrosine kinase  
CC (Flt-3 ligand). The invention is directed to enhancing the  
CC immune response of a vertebrate to an antigen or a cytokine by  
CC administering in vivo, into a tissue of a vertebrate, a Flt-3  
CC ligand-encoding polynucleotide, and 1 or more antigen- or  
CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding  
CC polynucleotide may encode the present full-length murine Flt-3  
CC ligand polypeptide, or amino acids 28-163, 1-163, 28-189 or 1-189  
CC of the Flt-3 ligand. The polynucleotides are incorporated into  
CC the cells of the vertebrate in vivo, and a prophylactically or  
CC therapeutically effective amount of Flt-3 ligand and 1 or more  
CC antigens or cytokines is produced in vivo. Pharmaceutical  
CC compositions comprising the polynucleotides are useful for  
CC suppressing tumour growth in a mammal. The tumour is melanoma,  
CC glioma or lymphoma, particularly B-cell lymphoma. They can also  
CC be used for the prophylactic and/or therapeutic treatment of:  
CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B  
CC and C in humans), parasitic (e.g. malaria) and fungal infections;  
CC (b) autoimmune diseases (e.g. rheumatoid arthritis and  
CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.  
CC Various other examples of these diseases are given in the  
CC specification.  
CC XX  
SQ Sequence 231 AA;  
Query Match 100.0%; Score 1223; DB 22; Length 231;  
Best Local Similarity 100.0%; Pred. No. 5, 2e-115;  
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MTVALAPAWSPNSLLILLSPCLRGTPDCYFSPHSPISSNFKYKFKRELTHLKDYPVT 60  
DB 1 MTVALAPAWSPNSLLILLSPCLRGTPDCYFSPHSPISSNFKYKFKRELTHLKDYPVT 60  
OY 61 VAVNLQDEKHCALMSLFLAQRWIEQLKTVAGSKMQLLEEDVNTIEHFVTSCTFQPLPEC 120  
DB 61 VAVNLQDEKHCALMSLFLAQRWIEQLKTVAGSKMQLLEEDVNTIEHFVTSCTFQPLPEC 120  
OY 121 LRFVQTNISHLKDTCTQLALAKPCIGKACQNSRCLEVCQCPDSSSTLLPPRSPIALBAT 180  
DB 121 LRFVQTNISHLKDTCTQLALAKPCIGKACQNSRCLEVCQCPDSSSTLLPPRSPIALBAT 180  
OY 181 ELPEPRPROQLLLLLPLTLVLLAAAGLWMORARRRGELHPGVPLPSHP 231  
DB 181 ELPEPRPROQLLLLLPLTLVLLAAAGLWMORARRRGELHPGVPLPSHP 231

RESULT 4  
AAR6177  
ID AAR6177 standard; Peptide: 232 AA.  
XX

AC AAR6177;  
XX XX 10-AUG-1995 (first entry)  
XX XX  
XX DE Mouse M0110/T118 Flt3 ligand peptide fragment.  
XX XX Flt3 ligand; tyrosine kinase receptor ligand.  
XX KM Homo sapiens.  
XX OS  
XX PN W09426891-A.  
XX PD 24-NOV-1994.  
XX PF 18-MAY-1994; 94WO-US05150.  
XX XX  
XX PR 19-MAY-1993; 93US-0065231.  
XX PR 07-JUL-1993; 93US-0089263.  
XX PR 16-JUL-1993; 93US-0092549.  
XX PR 13-AUG-1993; 93US-0106340.  
XX PR 24-AUG-1993; 93US-0112391.  
XX PR 19-NOV-1993; 93US-0155111.  
XX PR 03-DEC-1993; 93US-0162413.  
XX PA (INRM) INST NAT SANTE & RECH MEDICALE.  
XX PA (SCHE) SCHERING CORP.  
XX XX Birnbaum D, Culpepper JA, Hannum CH, Lee FD;  
XX DR WPI; 1995-006787/01.  
XX DR N-PSDB; AAO79464.  
XX XX  
XX PT New ligand for the Flt3 tyrosine kinase receptor - and related  
XX PT nucleic acid, vectors, host cells and antibodies, useful for  
XX PT treating abnormal cell physiology and proliferation, e.g. cancer,  
XX PT also for diagnosis and drug screening  
XX PS  
XX PS Claim 11; page 79-80; 90pp; English.  
XX XX  
CC A cDNA library from the human stromal cell line 293V48, in  
CC pME185, was screened with an 800 bp fragment derived from  
CC mouse clone T118. This fragment encompasses the coding region  
CC conserved between two mouse clones, T118 and T110. Approx. 20  
CC positive clones were selected and partially sequenced. Two  
CC clones, S86 and S109, were found to be approx. 75% homologous  
CC to the mouse clones over the first 163 AAs. Clone S86 continued  
CC to show homology to T110 until the stop codon, although to a  
CC lesser degree, for an overall homology of 66%. Clones T118 and  
CC S109 do not show homology to each other or to the other clones  
CC after mouse residue 163 (human residue 160). An additional mouse  
CC clone designated MB8 has a 29 AA insert at the junction between  
CC the common and divergent portions of the mouse ligand.  
CC XX  
SQ Sequence 232 AA;  
Query Match 99.1%; Score 1212.5; DB 16; Length 232;  
Best Local Similarity 99.6%; Pred. No. 6e-114;  
Matches 231; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
OY 1 MTVALAPAWSPNSLLILLSPCLRGTPDCYFSPHSPISSNFKYKFKRELTHLKDYPVT 60  
DB 1 MTVALAPAWSPNSLLILLSPCLRGTPDCYFSPHSPISSNFKYKFKRELTHLKDYPVT 60  
OY 61 VAVNLQDEKHCALMSLFLAQRWIEQLKTVAGSKMQLLEEDVNTIEHFVTSCTFQPLPEC 120  
DB 61 VAVNLQDEKHCALMSLFLAQRWIEQLKTVAGSKMQLLEEDVNTIEHFVTSCTFQPLPEC 120  
OY 121 LRFVQTNISHLKDTCTQLALAKPCIGKACQNSRCLEVCQCPDSSSTLLPPRSPIALBAT 180  
DB 121 LRFVQTNISHLKDTCTQLALAKPCIGKACQNSRCLEVCQCPDSSSTLLPPRSPIALBAT 180  
OY 181 ELPEPRPROQLLLLLPLTLVLLAAAGLWMORARRRGELHPGVPLPSHP 231  
DB 181 ELPEPRPROQLLLLLPLTLVLLAAAGLWMORARRRGELHPGVPLPSHP 231

Db 181 ELPEPRQQLLLLLLLPLTLVLLAAAWGLRMQARRRGELHGVPLPSHP 232

RESULT 5  
AAB20189  
ID AAB20189 standard; Protein: 232 AA.  
XX  
AC AAB20189;  
XX  
XX 14-MAY-2001 (first entry)  
XX  
XX Mouse Flt-3 ligand.  
XX  
XX  
XX Flt-3 ligand; fms-like tyrosine kinase; mouse; vaccine;  
KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;  
KW lymphoma; autoimmune disease; infection; gene therapy.  
XX  
XX Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..27  
FT /label= Signal\_peptide  
FT Protein 28..232  
FT /label= Mature\_protein  
FT Domain 28..188  
FT /label= Extracellular\_domain  
FT Domain 189..212  
FT /label= Transmembrane\_domain  
FT Domain 213..232  
FT /label= Cytoplasmic\_domain  
XX  
XX W0200109303-A2.  
XX  
XX 08-FEB-2001.  
XX  
XX 31-JUL-2000; 2000MO-US20679.  
XX  
XX 30-JUL-1999; 99US-0146170.  
XX  
XX (VICA-) VICAL INC.  
XX  
XX Hermanson CG;  
XX  
XX WPI: 2001-123319/13.  
XX  
XX N-PSDB; AAF30307.  
XX  
XX Immunogenic compositions comprising Flt-3 ligand encoding  
PT polynucleotide and one or more antigen, or cytokine encoding  
PT polynucleotides, useful for suppressing tumour growth and for treating  
PT autoimmune diseases (e.g. rheumatoid arthritis) -  
XX  
XX  
XX Claim 2; Page 125-126; 149pp; English.  
XX  
XX The present sequence is that of mouse fms-like tyrosine kinase  
CC (Flt-3 ligand). The invention is directed to enhancing the  
CC immune response of a vertebrate to an antigen or a cytokine by  
CC administering in vivo, into a tissue of a vertebrate, a Flt-3  
CC ligand-encoding polynucleotide, and 1 or more antigen- or  
CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding  
CC polynucleotide may encode the present sequence or the mature  
CC polypeptide. The polynucleotides are incorporated into  
CC the cells of the vertebrate in vivo, and a prophylactically or  
CC therapeutically effective amount of Flt-3 ligand and 1 or more  
CC antigens or cytokines is produced in vivo. Pharmaceutical  
CC compositions comprising the polynucleotides are useful for  
CC suppressing tumour growth in a mammal. The tumour is melanoma,  
CC glioma or lymphoma, particularly B-cell lymphoma. They can also  
CC be used for the prophylactic and/or therapeutic treatment of:  
CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B  
CC and C in humans), parasitic (e.g. malaria) and fungal infections;  
CC (b) autoimmune diseases (e.g. rheumatoid arthritis and  
CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.  
CC Various other examples of these diseases are given in the

CC specification.  
XX  
XX Sequence 232 AA:  
Query Match 98.8%; Score 1208.5; DB 22; Length 232;  
Best Local Similarity 99.1%; Pred. No. 1.5e-113;  
Matches 230; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
QY 1 MTVLAPAWSPNSSLLILLSPCLRGTPDCCFSHSPISSNFKVAFRELTHLKDYPVT 60  
Db 1 MTVLAPAWSPNSSLLILLSPCLRGTPDCCFSHSPISSNFKVAFRELTHLKDYPVT 60  
QY 61 VAVNLQDEHKCKALMSLFLAQRWIEQLKTVAGSKKQTLLEVDNFEIHFVTSCTOPPEEC 120  
Db 61 VAVNLQDEHKCKALMSLFLAQRWIEQLKTVAGSKKQTLLEVDNFEIHFVTSCTOPPEEC 120  
QY 121 LRFVOTNISHLLKDYCTOLLALKPCIGACQNFSSHLEVOQCPDPSSTLLPRSPALEAT 180  
Db 121 LRFVOTNISHLLKDYCTOLLALKPCIGACQNFSSHLEVOQCPDPSSTLLPRSPALEAT 180  
QY 181 ELPEPRPQQLLLLLLLPLTLVLLAAAWGLRMQARRRGELHGVPLPSHP 231  
Db 181 ELPEPRPQQLLLLLLLPLTLVLLAAAWGLRMQARRRGELHGVPLPSHP 232  
RESULT 6  
AAU02129  
ID AAU02129 standard; Protein: 288 AA.  
XX  
XX AAU02129;  
XX  
XX 29-AUG-2001 (first entry)  
XX  
XX  
XX Flt-3 ligand (FL) used to make chimeric immunogenic polypeptide.  
XX  
XX Mouse; granulocyte-macrophage-colony stimulating factor; GM-CSF;  
KW chimeric; heat shock protein; HSP; Flt-3 ligand; FL; exotoxin A;  
KW ETRA dit; antigenic; immunogenic; cytotoxic T cell response; tumour;  
KW vaccine; immunotherapy.  
XX  
XX Unidentified.  
XX  
XX W0200129233-A2.  
XX  
XX 26-APR-2001.  
XX  
XX 20-OCT-2000; 2000MO-US41422.  
XX  
XX 20-OCT-1999; 99US-0421608.  
XX  
XX 09-FEB-2000; 2000US-0501097.  
XX  
XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
XX Wu T, Hung C;  
XX  
XX WPI: 2001-290921/30.  
XX  
XX New chimeric polypeptide, useful as anti-tumour vaccines, comprises  
PT carboxy terminal fragment of heat shock protein, Flt-3 ligand or  
PT cytoplasmic translocation domain of Pseudomonas exotoxin A and  
PT antigenic polypeptide -  
XX  
XX  
XX Claim 9; Fig 19; 110pp; English.  
XX  
XX The sequence represents the amino acid sequence of Flt-3 ligand (FL)  
CC used in construction of a chimeric polypeptide comprising: (a) a first  
CC polypeptide domain containing a carboxy terminal fragment of a heat shock  
CC protein (HSP), an Flt-3 ligand (FL), a cytoplasmic translocation domain  
CC of a Pseudomonas exotoxin A (ETA dit), or a granulocyte-macrophage colony  
CC stimulating factor (GM-CSF); and (b) a second polypeptide domain  
CC containing an antigenic polypeptide. A composition comprising the  
CC chimeric polypeptide is useful for inducing an immune response such as a  
CC cytotoxic T cell response. The nucleic acid or vector encoding the



CC chimeric polypeptide present in the composition is administered as naked  
 CC DNA by gene gun or equivalent, or by liposomal formulation. These are  
 CC thus useful for vaccinating a mammal against infection by inducing an  
 CC immune response to a pathogen. Preferably they are useful for vaccinating  
 CC a mammal against a tumour antigen. The compositions and methods are  
 CC useful for stimulating or enhancing the immunogenicity of a selected  
 CC antigen or stimulating or enhancing a cellular immune response specific  
 CC for that antigen. The chimeric nucleic acid molecules and vaccination  
 CC methods, yield potent antigen-specific immunotherapy. The polynucleotides  
 CC and DNA vaccines can induce a cellular immune response that is at least  
 CC 40 fold more potent than conventional DNA vaccines. The vaccines are safe  
 CC and useful for administration to domesticated or agricultural animals, as  
 CC well as humans, and have low immunogenicity.

CC Sequence 288 AA:

Query Match 82.3%; Score 1006; DB 22; Length 288;  
 Best Local Similarity 99.5%; Pred. No. 5.3e-93;  
 Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPNSLLILLILSPCLRGPPDCYFSHSPISSENFVKRFELTDHLKDYPT 60  
 Db 1 MTVALPAMSPNSLLILLILSPCLRGPPDCYFSHSPISSENFVKRFELTDHLKDYPT 60  
 QY 61 VAVNLQDERKCKALMSFLAQRWTEOLKTVAAGSKMOTLEDVNTETHEFVTSCTFOPLPEC 120  
 Db 61 VAVNLQDERKCKALMSFLAQRWTEOLKTVAAGSKMOTLEDVNTETHEFVTSCTFOPLPEC 120  
 QY 121 LRFVQTNISHLKDTCTQLALAKPCIGKACONFSRCLEVCQPDSSSTLLPPRSPIALEAT 180  
 Db 121 LRFVQTNISHLKDTCTQLALAKPCIGKACONFSRCLEVCQPDSSSTLLPPRSPIALEAT 180  
 QY 181 ELPEPRPROL 190  
 Db 181 ELPEPRPROL 190

RESULT 7  
 AAB20187  
 ID AAB20187 standard; Protein: 189 AA.

AC AAB20187;  
 XX  
 DT 14-MAY-2001 (first entry)  
 XX  
 DE Mouse Flt-3 ligand (secreted form).  
 XX  
 KW Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;  
 KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;  
 KW lymphoma; autoimmune disease; infection; gene therapy.  
 XX  
 OS Mus musculus.

XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..27  
 FT Protein /label= signal\_peptide  
 FT 28..189  
 XX /label= Mature\_protein

PN WO200109303-A2.  
 XX  
 PD 08-FEB-2001.  
 XX  
 PF 31-JUL-2000; 2000WO-US20679.  
 XX  
 PR 30-JUL-1999; 99US-0146170.  
 XX  
 PA (VICA-) VICAL INC.  
 XX  
 PI Hermanson GG;  
 XX  
 DR WPI: 2001-123319/13.  
 DR N-PSDB; AAF30305, AAF30313.

XX Immunogenic compositions comprising Flt-3 ligand encoding  
 PT polynucleotide and one or more antigen, or cytokine encoding  
 PT polynucleotides, useful for suppressing tumour growth and for treating  
 PT autoimmune diseases (e.g. rheumatoid arthritis) -  
 XX  
 PS Claim 2; Page 121; 149pp; English.

XX  
 CC The present sequence is that of a secreted form of mouse Fms-like  
 CC tyrosine kinase (Flt-3 ligand), lacking the transmembrane and  
 CC cytoplasmic domains of the full-length form (see AAB20186). This  
 CC secreted form of the Flt-3 ligand is expressed by vector VR6200  
 CC (see AAF30313). The invention is directed to enhancing the  
 CC immune response of a vertebrate to an antigen or a cytokine by  
 CC administering in vivo, into a tissue of a vertebrate, a Flt-3  
 CC ligand-encoding polynucleotide, such as VR6200, and 1 or more  
 CC antigen- or cytokine-encoding polynucleotides. The polynucleotides  
 CC are incorporated into the cells of the vertebrate in vivo, and a  
 CC prophylactically or therapeutically effective amount of Flt-3  
 CC ligand and 1 or more antigens or cytokines is produced in vivo.  
 CC Pharmaceutical compositions comprising the polynucleotides are  
 CC useful for suppressing tumour growth in a mammal. The tumour is  
 CC melanoma, glioma or lymphoma, particularly B-cell lymphoma. The  
 CC co-injection of VR6200 and tumour-specific antigen-encoding plasmid  
 CC VR1623 into mice significantly enhanced protection from tumour  
 CC challenge. The claimed pharmaceutical compositions can also be  
 CC used for the prophylactic and/or therapeutic treatment of:  
 CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B  
 CC and C in humans), parasitic (e.g. malaria) and fungal infections;  
 CC (b) autoimmune diseases (e.g. rheumatoid arthritis and  
 CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.  
 CC Various other examples of these diseases are given in the  
 CC specification.

CC Sequence 189 AA:

Query Match 82.1%; Score 1004; DB 22; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-93;  
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPNSLLILLILSPCLRGTPDCYFSHSPISSENFVKRFELTDHLKDYPT 60  
 Db 1 MTVALPAMSPNSLLILLILSPCLRGTPDCYFSHSPISSENFVKRFELTDHLKDYPT 60  
 QY 61 VAVNLQDERKCKALMSFLAQRWTEOLKTVAAGSKMOTLEDVNTETHEFVTSCTFOPLPEC 120  
 Db 61 VAVNLQDERKCKALMSFLAQRWTEOLKTVAAGSKMOTLEDVNTETHEFVTSCTFOPLPEC 120  
 QY 121 LRFVQTNISHLKDTCTQLALAKPCIGKACONFSRCLEVCQPDSSSTLLPPRSPIALEAT 180  
 Db 121 LRFVQTNISHLKDTCTQLALAKPCIGKACONFSRCLEVCQPDSSSTLLPPRSPIALEAT 180  
 QY 181 ELPEPRPRO 189  
 Db 181 ELPEPRPRO 189

RESULT 8  
 AAB20191  
 ID AAB20191 standard; Protein: 172 AA.

XX  
 AC AAB20191;  
 XX  
 DT 14-MAY-2001 (first entry)  
 XX  
 DE Mouse Flt-3 ligand.

XX  
 KW Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;  
 KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;  
 KW lymphoma; autoimmune disease; infection; gene therapy.  
 XX  
 OS Mus musculus.

```

FH Key Location/Qualifiers
FT Peptide 1..27
FT /label= signal_peptide
FT 28..172
FT Protein /label= Mature_protein
FT
FN WO200109303-A2.
FN
PD 08-FEB-2001.
PD
PF 31-JUL-2000; 2000WO-US20679.
PF
PR 30-JUL-1999; 99US-0146170.
PR
PA (VICA-) VICAL INC.
PA
PI Hermanson GG;
PI
XX WPI: 2001-123319/13.
XX
XX N-PSDB; AAF30309.
XX
XX Immunogenic compositions comprising Flt-3 ligand encoding
XX polynucleotide and one or more antigen, or cytokine encoding
XX polynucleotides, useful for suppressing tumour growth and for treating
XX autoimmune diseases (e.g. rheumatoid arthritis) -
XX
XX Claim 2; Page 130; 149pp; English.
XX
XX The present sequence is that of mouse Fms-like tyrosine kinase
XX (Flt-3 ligand). The invention is directed to enhancing the
XX immune response of a vertebrate to an antigen or a cytokine by
XX administering in vivo, into a tissue of a vertebrate, a Flt-3
XX ligand-encoding polynucleotide, and 1 or more antigen- or
XX cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
XX polynucleotide may encode the present sequence or the mature
XX polypeptide. The polynucleotides are incorporated into
XX the cells of the vertebrate in vivo, and a prophylactically or
XX therapeutically effective amount of Flt-3 ligand and 1 or more
XX antigens or cytokines is produced in vivo. Pharmaceutical
XX compositions comprising the polynucleotides are useful for
XX suppressing tumour growth in a mammal. The tumour is melanoma,
XX glioma or lymphoma, particularly B-cell lymphoma. They can also
XX be used for the prophylactic and/or therapeutic treatment of:
XX (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
XX and C in humans), parasitic (e.g. malaria) and fungal infections;
XX (b) autoimmune diseases (e.g. rheumatoid arthritis and
XX osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
XX Various other examples of these diseases are given in the
XX specification.
XX
XX Sequence 172 AA:
XX
XX Query Match 71.9%; Score 879; DB 22; Length 172;
XX Best Local Similarity 98.2%; Pred. No. 1.7e-80;
XX Matches 165; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 MTVLAPAMSPNSILLILLISPLCRGTPDCYFHSHPISSNFKVFKRELTDHLKDYPT 60
XX |||||||
XX Db 1 MTVLAPAMSPNSILLILLISPLCRGTPDCYFHSHPISSNFKVFKRELTDHLKDYPT 60
XX
XX 61 VAVNIODEKHCKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTLHFVTSCTFQPLPEC 120
XX |||||||
XX QY 61 VAVNIODEKHCKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTLHFVTSCTFQPLPEC 120
XX |||||||
XX Db 61 VAVNIODEKHCKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTLHFVTSCTFQPLPEC 120
XX |||||||
XX QY 121 LRFVQNIISHLKDTCTOLIAKPCIGKACONFSRCLEVOCCDDSTL 168
XX |||||||
XX Db 121 LRFVQNIISHLKDTCTOLIAKPCIGKACONFSRCLEVOCCDDSTL 168
XX |||||||
XX
XX RESULT 9
XX AAB20188-
XX ID AAB20188 standard; Protein; 220 AA.
XX

```

```

AC AAB20188;
XX
XX 14-MAY-2001 (first entry)
XX
XX Mouse Flt-3 ligand.
XX
XX Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
XX immunotherapy; therapy; tumour; cancer; melanoma; glioma;
XX lymphoma; autoimmune disease; infection; gene therapy.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Peptide 1..27
XX /label= signal_peptide
XX 28..220
XX Protein /label= Mature_protein
XX
XX WO200109303-A2.
XX
XX 08-FEB-2001.
XX
XX 31-JUL-2000; 2000WO-US20679.
XX
XX 30-JUL-1999; 99US-0146170.
XX
XX (VICA-) VICAL INC.
XX
XX Hermanson GG;
XX
XX WPI: 2001-123319/13.
XX
XX N-PSDB; AAF30306.
XX
XX Immunogenic compositions comprising Flt-3 ligand encoding
XX polynucleotide and one or more antigen, or cytokine encoding
XX polynucleotides, useful for suppressing tumour growth and for treating
XX autoimmune diseases (e.g. rheumatoid arthritis) -
XX
XX Claim 2; Page 123-124; 149pp; English.
XX
XX The present sequence is that of mouse Fms-like tyrosine kinase
XX (Flt-3 ligand). The invention is directed to enhancing the
XX immune response of a vertebrate to an antigen or a cytokine by
XX administering in vivo, into a tissue of a vertebrate, a Flt-3
XX ligand-encoding polynucleotide, and 1 or more antigen- or
XX cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
XX polynucleotide may encode the present sequence or the mature
XX polypeptide. The polynucleotides are incorporated into
XX the cells of the vertebrate in vivo, and a prophylactically or
XX therapeutically effective amount of Flt-3 ligand and 1 or more
XX antigens or cytokines is produced in vivo. Pharmaceutical
XX compositions comprising the polynucleotides are useful for
XX suppressing tumour growth in a mammal. The tumour is melanoma,
XX glioma or lymphoma, particularly B-cell lymphoma. They can also
XX be used for the prophylactic and/or therapeutic treatment of:
XX (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
XX and C in humans), parasitic (e.g. malaria) and fungal infections;
XX (b) autoimmune diseases (e.g. rheumatoid arthritis and
XX osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
XX Various other examples of these diseases are given in the
XX specification.
XX
XX Sequence 220 AA:
XX
XX Query Match 71.9%; Score 879; DB 22; Length 220;
XX Best Local Similarity 82.3%; Pred. No. 2.4e-80;
XX Matches 177; Conservative 5; Mismatches 21; Indels 12; Gaps 3;
XX
XX 1 MTVLAPAMSPNSILLILLISPLCRGTPDCYFHSHPISSNFKVFKRELTDHLKDYPT 60
XX |||||||
XX Db 1 MTVLAPAMSPNSILLILLISPLCRGTPDCYFHSHPISSNFKVFKRELTDHLKDYPT 60
XX |||||||
XX QY 61 VAVNIODEKHCKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTLHFVTSCTFQPLPEC 120
XX |||||||
XX

```

```

Db      61 VAVNLQDEKHKCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120
Oy      121 LRFVQNTINSHLKDTCOTLLALPCIGKACONFSRCLEVOCCOPSTLLPPRS----PIA 176
Db      121 LRFVQNTINSHLKDTCOTLLALPCIGKACONFSRCLEVOCCOPGNG---GPRQHHGATR 177
Oy      177 LEATELPEPRPRQLLL-----LLLLPLTVLLAA 206
Db      178 LRTATALLTWCPCGLLPLVGTSHMFPLPYFLSFLSS 212

RESULT 10
AAB20190
ID      AAB20190 standard; Protein: 220 AA.
XX
AC      AAB20190;
XX
Df      14-MAY-2001 (first entry)
XX
DE      Mouse Flt-3 ligand.
XX
KW      Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
KW      immunotherapy; therapy; tumour; cancer; melanoma; glioma;
OS      lymphoma; autoimmune disease; infection; gene therapy.
XX
Mus musculus.
XX
FH      Key Location/Qualifiers
FT      Peptide 1..27
FT      /label= Signal_peptide
FT      /label= Mature_protein
XX
XX      Protein 28..220
XX
XX      MO200109303-A2.
XX
XX      08-FEB-2001.
XX
XX      31-JUL-2000; 2000MO-US20679.
XX
XX      30-JUL-1999; 99US-0146170.
XX
XX      (VIC- ) VICAL INC.
XX
XX      Hermanson GG;
XX
XX      WPI; 2001-123319/13.
XX      N-PSDB; AAF30308.
XX
XX      Immunogenic compositions comprising Flt-3 ligand encoding
XX      polynucleotides, useful for suppressing tumour growth and for treating
XX      autoimmune diseases (e.g. rheumatoid arthritis) -
XX
XX      Claim 2; Page 128; 149pp; English.
XX
XX      The present sequence is that of mouse Fms-like tyrosine kinase
XX      (Flt-3 ligand). The invention is directed to enhancing the
XX      immune response of a vertebrate to an antigen or a cytokine by
XX      administering in vivo, into a tissue of a vertebrate, a Flt-3
XX      ligand encoding polynucleotides, and 1 or more antigen- or
XX      cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
XX      polynucleotide may encode the present sequence or the mature
XX      polypeptide. The polynucleotides are incorporated into
XX      the cells of the vertebrate in vivo, and a prophylactically or
XX      therapeutically effective amount of Flt-3 ligand and 1 or more
XX      antigens or cytokines is produced in vivo. Pharmaceutical
XX      compositions comprising the polynucleotides are produced for
XX      suppressing tumour growth in a mammal. The tumour is melanoma,
XX      glioma or lymphoma, particularly B-cell lymphoma. They can also
XX      be used for the prophylactic and/or therapeutic treatment of:
XX      (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
XX      and C in humans), parasitic (e.g. malaria) and fungal infections;

```

```

CC      (b) autoimmune diseases (e.g. rheumatoid arthritis and
CC      osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
CC      Various other examples of these diseases are given in the
CC      specification.
XX
SQ      Sequence 220 AA:
XX
Query Match 71.9%; Score 879; Db 22; Length 220;
Best Local Similarity 82.3%; Pred. No. 2,4e-80;
Matches 177; Conservative 5; Mismatches 21; Indels 12; Gaps 3;
Oy      1 MTVLAPAMSPNSLLLLLLSPCLRGTPDCYFSHSPISSNFKYKFFELTDHLKRYPT 60
Db      1 MTVLAPAMSPNSLLLLLLSPCLRGTPDCYFSHSPISSNFKYKFFELTDHLKRYPT 60
Oy      61 VAVNLQDEKHKCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120
Db      61 VAVNLQDEKHKCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120
Oy      121 LRFVQNTINSHLKDTCOTLLALPCIGKACONFSRCLEVOCCOPSTLLPPRS----PIA 176
Db      121 LRFVQNTINSHLKDTCOTLLALPCIGKACONFSRCLEVOCCOPGNG---GPRQHHGATR 177
Oy      177 LEATELPEPRPRQLLL-----LLLLPLTVLLAA 206
Db      178 LRTATALLTWCPCGLLPLVGTSHMFPLPYFLSFLSS 212

RESULT 11
AA58204
ID      AA58204 standard; Protein: 294 AA.
XX
XX      AA58204;
XX
XX      14-MAR-2000 (first entry)
XX
XX      Canine Flt-3 ligand.
XX
XX      Flt-3 ligand; antibody; canine; feline; inhibitor; immune response;
XX      immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX
XX      Canis familiaris.
XX
XX      WO9961618-A2.
XX
XX      02-DEC-1999.
XX
XX      28-MAY-1999; 99WO-US11942.
XX
XX      29-MAY-1999; 98US-0087306.
XX
XX      (HESK-) HESKA CORP.
XX
XX      Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
XX      WPI; 2000-072623/06.
XX      N-PSDB; AA255487, AA255488, AA255489, AA255490.
XX
XX      Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX      useful for treating or preventing e.g. tumors or autoimmune disease
XX
XX      Claim 3b; Page 159-160; 264pp; English.
XX
XX      Sequences AA58204 and AA58206-Y58209 reselectively represent
XX      encoded, mature, clone 1 and clone 19 canine Flt-3 ligand, while
XX      sequences AA58210-Y58211 represent encoded and mature feline Flt-3
XX      ligand. The invention relates to canine interleukin-4 (IL-4) or
XX      canine or feline Flt-3 ligand, canine or feline CD40, canine or
XX      feline CD134 (CD40 ligand), canine IL-5, canine IL-13, feline
XX      interferon-alpha (IFN-alpha) and feline granulocyte macrophage
XX      colony-stimulating factor (GM-CSF), and nucleotides which encode these
XX      immunoregulatory proteins. The proteins, and their associated
XX      nucleic acids, specific antibodies and inhibitors may be used as

```



XX PF 31-JUL-2000; 2000WO-US20679.  
XX PR 30-JUL-1999; 99US-0146170.  
XX PA (VIC-1) VICAL INC.  
XX PI Hermanson GG;  
XX DR WPI: 2001-123319/13.  
XX DR N-PSDB: AAF30312.  
XX PT Immunogenic compositions comprising Flt-3 ligand encoding  
XX PT polynucleotide and one or more antigen, or cytokine encoding  
XX PT polynucleotides, useful for suppressing tumour growth and for treating  
XX PT autoimmune diseases (e.g. rheumatoid arthritis) -  
XX PS Claim 2; Page 137-138; 149pp; English.  
XX CC The present sequence is that of human Fms-like tyrosine kinase  
XX CC (Flt-3 ligand). The invention is directed to enhancing the  
XX CC immune response of a vertebrate to an antigen or a cytokine by  
XX CC administering in vivo, into a tissue of a vertebrate, a Flt-3  
XX CC ligand-encoding polynucleotide, and 1 or more antigen- or  
XX CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding  
XX CC polynucleotide may encode the present full-length human Flt-3  
XX CC ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-235  
XX CC of the Flt-3 ligand. The polynucleotides are incorporated into  
XX CC the cells of the vertebrate in vivo, and a prophylactically or  
XX CC therapeutically effective amount of Flt-3 ligand and 1 or more  
XX CC antigens or cytokines is produced in vivo. Pharmaceutical  
XX CC compositions comprising the polynucleotides are useful for  
XX CC suppressing tumour growth in a mammal. The tumour is melanoma,  
XX CC glioma or lymphoma, particularly B-cell lymphoma. They can also  
XX CC be used for the prophylactic and/or therapeutic treatment of:  
XX CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B  
XX CC and C in humans), parasitic (e.g. malaria) and fungal infections;  
XX CC (b) autoimmune diseases (e.g. rheumatoid arthritis and  
XX CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.  
XX CC Various other examples of these diseases are given in the  
XX CC specification.  
XX SQ Sequence 235 AA;  
Query Match 63.2%; Score 772.5; DB 22; Length 235;  
Best Local Similarity 70.7%; Pred. No. 1.4e-69;  
Matches 164; Conservative 17; Mismatches 42; Indels 9; Gaps 4;  
OY 1 MTVLAPAMSPNSLLLLLSPLRGTPDCYFESHSPISSNFVKFRELTHLKDYPVT 60  
DB 1 MTVLAPAMSP-TTYLLLLLSGLSGTDCSPFQHSPISSDFAVKIRELSDYLLDQYPT 59  
OY 61 VAVNLODEKCKALMSFLAQRWIEOLKTYAGSKMOTLEDVNTETHFVTSCTFPQPEEC 120  
DB 60 VASNIODEELCGALMRLVLAQRWIERLKYAGSKMGLLEVRNTEIHFVTKCAFQPPSC 119  
OY 121 LRFVOTNISHLKDPCTQTLALKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSPALBAT 180  
DB 120 LRFVOTNISRLQETSQVALKPMWTR--QNFSCLELQCCPDSSSTLLPPRSPALBAT 177  
OY 181 ELPEPRRQQLLLLLPLPLVLVLAAMGLRMQKARRR---GELHPGVLP 228  
DB 178 APTAPQPP--LLLLLLPVGLLLAAMCCLHWQTRRRTPRPEQVPVPSP 227  
RESULT 14  
AAR67541  
ID AAR67541 standard; Protein: 235 AA.  
XX AAR67541;  
XX AC  
XX DT 05-AUG-1995 (first entry)  
XX

DE Human flt-3 ligand.  
XX Flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX FT Peptide 1..26  
XX FT /label= Sig-peptide  
XX FT /note= "signal peptide may extend to position 27"  
XX FT Domain 27..182  
XX FT /label= Extracellular domain  
XX FT /note= "extracellular domain may start at  
XX FT position 28"  
XX FT Domain 183..205  
XX FT /label= Transmembrane domain  
XX FT Domain 206..235  
XX FT /label= Cytoplasmic domain  
XX PN EPE27487-A.  
XX PD 07-DEC-1994.  
XX PF 19-MAY-1994; 94EP-0303575.  
XX PF 24-MAY-1993; 93US-0068394.  
XX PR 12-AUG-1993; 93US-0106463.  
XX PR 25-AUG-1993; 93US-0111758.  
XX PR 03-DEC-1993; 93US-0162407.  
XX PR 07-MAR-1994; 94US-0209502.  
XX PR 11-MAY-1994; 94US-0243545.  
XX PA (IMM V) IMMUNEX CORP.  
XX PI Beckmann MP, Lyman SD;  
XX DR WPI: 1995-008071/02.  
XX DR N-PSDB: AAQ79079.  
XX DR 1995-008071/02.  
XX PT Isolated ligands for flt 3 receptors - useful for treating  
XX PT anaemia, AIDS and various cancers  
XX PS Disclosure; Page 29-30; 33pp; English.  
XX CC A human T-cell lambda-gt10 random primed cDNA library was  
XX CC screened with a fragment corresponding to the extracellular  
XX CC domain of mouse flt3 ligand (flt3-L) (nt 103-516 of AAQ79076)  
XX CC to isolate human flt3-L cDNA. Flt-3 stimulates progenitor and  
XX CC stem cells, and can be used e.g. in gene therapy protocols.  
XX SQ Sequence 235 AA;  
Query Match 62.8%; Score 768.5; DB 16; Length 235;  
Best Local Similarity 70.3%; Pred. No. 3.6e-69;  
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;  
OY 1 MTVLAPAMSPNSLLLLLSPLRGTPDCYFESHSPISSNFVKFRELTHLKDYPVT 60  
DB 1 MTVLAPAMSP-TTYLLLLLSGLSGTDCSPFQHSPISSDFAVKIRELSDYLLDQYPT 59  
OY 61 VAVNLODEKCKALMSFLAQRWIEOLKTYAGSKMOTLEDVNTETHFVTSCTFPQPEEC 120  
DB 60 VASNIODEELCGALMRLVLAQRWIERLKYAGSKMGLLEVRNTEIHFVTKCAFQPPSC 119  
OY 121 LRFVOTNISHLKDPCTQTLALKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSPALBAT 180  
DB 120 LRFVOTNISRLQETSQVALKPMWTR--QNFSCLELQCCPDSSSTLLPPRSPALBAT 177  
OY 181 ELPEPRRQQLLLLLPLPLVLVLAAMGLRMQKARRR---GELHPGVLP 228  
DB 178 APTAPQPP--LLLLLLPVGLLLAAMCCLHWQTRRRTPRPEQVPVPSP 227

## RESULT 15

AAW67769  
ID AAW67769 standard: Protein: 235 AA.

XX AC AAW67769;

XX DT 25-MAR-1999 (first entry)

XX DE Human flt3-ligand.

XX KW Antigen-specific peripheral immune tolerance: flt3-ligand; flt3-L;  
KW immunogenic; autoimmune disease; organ transplantation; food allergy;  
KW tissue transplantation.

XX OS Homo sapiens.

XX PN W09857655-A1.

XX PD 23-DEC-1998.

XX PF 12-JUN-1998; 98WO-US12085.

XX PR 17-JUN-1997; 97US-0877421.

XX PA (IMMUNEX CORP.

XX PI Abbott NM, Mowat AM, Viney JL;

XX DR WPI: 1999-070422/06.

XX DR N-PSDB: AAV81506.

XX PT Methods for initiating or enhancing antigen specific immune  
XX tolerance - by using murine or human flt3 ligand

XX PS Claim 1; Page 14-15; 25pp: English.

XX CC A method has been developed of initiating or enhancing: (i) an antigen-  
CC specific immune tolerance; or (ii) immunotolerance of a therapeutic  
CC immunogenic molecule by addition of a polypeptide, before, after or with  
CC the mucosal administration of an immunotolerizing amount of the antigen  
CC or therapeutic molecule, respectively. The polypeptide is capable of  
CC binding the flt3 receptor and is: a) amino acids 28-x of murine flt3  
CC ligand (flt3-L), where x is an amino acid between 163-231; b) amino  
CC acids 28-y of human flt3-L, where y is an amino acid between 160-235;  
CC and c) a polypeptide that has at least 90% identity to the polypeptides  
CC of either (a) or (b). The method ameliorates the effects of autoimmune  
CC diseases, food allergies or organ or tissue rejection following  
CC transplantation. Administration of flt3-L allows lower doses of antigens  
CC to be used in vivo for mucosally administered antigens. The present  
CC sequence represents human flt3-L.  
XX SQ

XX Sequence 235 AA;

Query Match 62.8%; Score 768.5; DB 20; Length 235;

Best Local Similarity 70.3%; Pred. No. 3.6e-69;

Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

OY 1 MTVLAPAMSPNSLLILLILLLSPCLRGPPDCYFSHSPISSNFKKFRRLTDHLKDDPYPT 60

DB 1 MTVLAPAMSP-TTYLLILLILLLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLDIDYPT 59

OY 61 VAVNIQDKRKCKALMSLFIAQRMIEQLTKVAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 120

DB 60 VASNIQDKRKCKALMSLFIAQRMIEQLTKVAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 119

OY 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFESKCLEVQCQPSSTLLPPRPIALEAT 180

DB 120 LRFVQTNISHLKDTCTQLALKPCIGKACQNFESKCLEVQCQPSSTLLPPRPIALEAT 177

OY 181 ELPEPRRQLLLILLPLTLVLLAAAGLRFQRRARR---GELHPCVPLP 228

DB 178 APTAPQPP-LTLLLLPVGILLLLAAACLMWRQRRRRTPRRGQVPPVPS 227

Search completed: November 24, 2002, 10:10:13  
Job time : 32.2296 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 24, 2002, 10:11:46 ; Search time 8.42704 Seconds  
(without alignments)  
429.309 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223

Sequence: 1 MTVLAPAMSPNSLLLLLLL.....WQRRRRGELHPGVLPDPSHP 231

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, AA:  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PC1\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/PC1US\_PUBCOMB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1223	100.0	231	9	US-10-095-449-2
2	1223	100.0	231	10	US-09-448-378-2
3	1223	100.0	231	10	US-09-983-806-2
4	768.5	62.8	235	9	US-10-095-449-6
5	768.5	62.8	235	10	US-09-448-378-1
6	768.5	62.8	235	10	US-09-983-806-6
7	768.5	62.8	235	10	US-09-904-536-1
8	724.5	59.2	137	10	US-09-904-536-19
9	692	56.6	212	10	US-09-904-536-10
10	687	56.1	209	10	US-09-904-536-15
11	686	56.1	209	10	US-09-904-536-14
12	685	56.1	209	10	US-09-904-536-18
13	685	56.0	209	10	US-09-904-536-16
14	682	55.8	209	10	US-09-904-536-9
15	682	55.8	209	10	US-09-904-536-12
16	682	55.8	209	10	US-09-904-536-17
17	680	55.6	209	10	US-09-904-536-11
18	679	55.5	209	10	US-09-904-536-13
19	678	55.4	209	10	US-09-904-536-8

20	95.5	7.8	909	10	US-09-867-852-142	Sequence 142, App
21	94	7.7	355	10	US-09-948-018-2	Sequence 2, Appl1
22	92	7.5	885	10	US-09-867-852-2	Sequence 2, Appl1
23	89.5	7.3	874	10	US-09-826-508-26	Sequence 26, Appl1
24	89.5	7.3	941	9	US-09-793-139-47	Sequence 47, Appl1
25	89.5	7.3	941	10	US-09-818-879-47	Sequence 47, Appl1
26	89.5	7.3	941	10	US-09-211-755B-47	Sequence 47, Appl1
27	80.5	6.6	391	10	US-09-800-729-208	Sequence 208, App
28	80.5	6.6	395	9	US-09-987-107-35	Sequence 35, Appl1
29	80	6.5	811	9	US-09-992-598-57	Sequence 57, Appl1
30	80	6.5	811	10	US-09-187-368-1	Sequence 1, Appl1
31	80	6.5	811	10	US-09-989-722-57	Sequence 57, Appl1
32	80	6.5	811	10	US-09-989-722-57	Sequence 57, Appl1
33	80	6.5	811	10	US-09-989-729-57	Sequence 57, Appl1
34	80	6.5	811	10	US-09-989-727-57	Sequence 57, Appl1
35	80	6.5	811	10	US-09-989-731-57	Sequence 57, Appl1
36	80	6.5	811	10	US-09-989-732-57	Sequence 57, Appl1
37	80	6.5	811	10	US-09-991-073-57	Sequence 57, Appl1
38	80	6.5	811	10	US-09-990-442-57	Sequence 57, Appl1
39	80	6.5	811	10	US-09-991-163-57	Sequence 57, Appl1
40	80	6.5	811	10	US-09-993-604-57	Sequence 57, Appl1
41	80	6.5	811	10	US-09-990-456-57	Sequence 57, Appl1
42	80	6.5	811	10	US-09-989-721-57	Sequence 57, Appl1
43	80	6.5	811	12	US-10-052-586-414	Sequence 414, App
44	79.5	6.5	365	10	US-09-867-550-2026	Sequence 2026, App
45	77.5	6.3	929	9	US-09-793-139-4	Sequence 4, Appl1

## ALIGNMENTS

RESULT 1  
US-10-095-449-2  
; Sequence 2, Application US/10095449  
; Patent No. US20020160004A1  
GENERAL INFORMATION:  
APPLICANT: Lyman, Stewart D.  
Beckmann, M. Patricia  
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.0.1  
SOFTWARE: Microsoft Word, Version #5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/095,449  
FILING DATE: 13-Mar-2002  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/669,692  
FILING DATE: 24-JUN-1996  
APPLICATION NUMBER: US/08/162,407  
FILING DATE: December 3, 1993  
APPLICATION NUMBER: 08/111,758  
FILING DATE: August 25, 1993  
APPLICATION NUMBER: 08/106,463  
FILING DATE: August 12, 1993  
APPLICATION NUMBER: 08/068,394  
FILING DATE: May 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2813-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430

```

? TELEFAX: (206) 233-0644
?
? TELEX: 756822
?
? INFORMATION FOR SEQ ID NO: 2:
?
?   SEQUENCE CHARACTERISTICS:
?     LENGTH: 231 amino acids
?     TYPE: amino acid
?     TOPOLOGY: linear
?
? MOLECULE TYPE: protein
?
? SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-095-449-2
```

Query Match	100.0%;	Score 1223;	DB 9;	Length 231;
Best Local Similarity	100.0%;	Pred. No. 1.5e-107;		
Matches 231; Conservative	0;	Mismatches	0;	Indels 0; Gaps

	QY	Db	QY	Db	QY	Db	QY	Db	QY	Db
1	MTVLAPAPSPSSLLLLLLLSPLCRGPDCYFSHSPISSNFKKAPFELDLHKQVPT	60	1	MTVLAPAPSPSSLLLLLLLSPLCRGPDCYFSHSPISSNFKKAPFELDLHKQVPT	60	1	MTVLAPAPSPSSLLLLLLLSPLCRGPDCYFSHSPISSNFKKAPFELDLHKQVPT	60	1	MTVLAPAPSPSSLLLLLLLSPLCRGPDCYFSHSPISSNFKKAPFELDLHKQVPT
61	VAVNLQDERHCKALMSLFLLQRMIEQLKTYAGSKMQLLLEDVNIETHFVSTCFQPIPEC	120	61	VAVNLQDERHCKALMSLFLLQRMIEQLKTYAGSKMQLLLEDVNIETHFVSTCFQPIPEC	120	61	VAVNLQDERHCKALMSLFLLQRMIEQLKTYAGSKMQLLLEDVNIETHFVSTCFQPIPEC	120	61	VAVNLQDERHCKALMSLFLLQRMIEQLKTYAGSKMQLLLEDVNIETHFVSTCFQPIPEC
181	ELRPPRPQQLLLLLLLLPRTLVLVLAAMWGLRMQARRRGELHREVPRLPSNP	231	181	ELRPPRPQQLLLLLLLLPRTLVLVLAAMWGLRMQARRRGELHREVPRLPSNP	231	181	ELRPPRPQQLLLLLLLLPRTLVLVLAAMWGLRMQARRRGELHREVPRLPSNP	231	181	ELRPPRPQQLLLLLLLLPRTLVLVLAAMWGLRMQARRRGELHREVPRLPSNP

```

RESULT 2
US-09-448-378-2
; Sequence 2, Application US/09448378
; Patent No. US2002003451A1
; GENERAL INFORMATION:
; APPLICANT: Brasel, Kenneth
; TITLE OF INVENTION: Dendritic Cell Stimulatory Factor
; FILE REFERENCE: 2836-D
; CURRENT APPLICATION NUMBER: US/09/448,378
; CURRENT FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Mus sp.
; US-09-448-378-2

```

Query Match	100.0%	Score 1223	DB 10	Length 231
Best Local Similarity	100.0%	Pred. No. 1	5e-107	
Matches 231	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MTVLAAPMSFNSLLILLILSPCLRGTPDCYFSHSP1SSNFVKVKEFELTDHLKQDPVT	60	
Db	1	MTVLAAPMSFNSLLILLILSPCLRGTPDCYFSHSP1SSNFVKVKEFELTDHLKQDPVT	60	
QY	61	VAVNIDDEKHKRKLMSLFLAQRWIDQLTVGSKKQTLLEPVNEIHFVTSCTFOPLRPEC	120	
Db	61	VAVNIDDEKHKRKLMSLFLAQRWIDQLTVGSKKQTLLEPVNEIHFVTSCTFOPLRPEC	120	
QY	121	LRFVQTNISHLKLDKDTOTLLALPCIGRACQNFSCLEVCQCPDPSSTLPPRSPIALEAT	180	
Db	121	LRFVQTNISHLKLDKDTOTLLALPCIGRACQNFSCLEVCQCPDPSSTLPPRSPIALEAT	180	
QY	181	ELREPPRRQULLLLILLPLTVLLAANGKLKQRRRRRGELHREVPPLRPSHP	231	
Db	181	ELREPPRRQULLLLILLPLTVLLAANGKLKQRRRRRGELHREVPPLRPSHP	231	

RESULT 3  
US-09-983-805-2

Sequence 2, Application US/09983806  
Patent No. US20020107365A1  
GENERAL INFORMATION:  
APPLICANT: Lyman, Stewart D.  
Beckmann, M. Patricia  
TITLE OF INVENTION: Ligands for Flt3/Flk-2 Receptors  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.0.1  
SOFTWARE: Microsoft Word, Version #5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/983, 806  
FILING DATE: 25-Oct-2001  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/444, 626  
FILING DATE: 19-MAY-1995  
APPLICATION NUMBER: US 08/162, 407  
FILING DATE: 03-DEC-1993  
APPLICATION NUMBER: 08/111, 758  
FILING DATE: August 25, 1993  
APPLICATION NUMBER: 08/106, 463  
FILING DATE: August 12, 1993  
APPLICATION NUMBER: 08/068, 394  
FILING DATE: May 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2813-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 231 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
IS-09-983-806-2

Query Match	100.0%;	Score 1223;	DB 10;	Length 231;
Best Local Similarity	100.0%;	Pred. No. 1.5e-107;		
Matches 231; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MYVLAAPMSPNSSLLIIIIIIISPCIRGPPDCYFHSHSISSNFYVKRRELTDLHKDLYPT	60
Db	1	MYVLAAPMSPNSSLLIIIIIIISPCIRGPPDCYFHSHSISSNFYVKRRELTDLHKDLYPT	60
QY	61	VAVNLODEKHCKALMSLELAORMIEBOLKTVAAGSKMOTLIEDVNTIEHFTVSCFPQPLEEC	120
Db	61	VAVNLODEKHCKALMSLELAORMIEBOLKTVAAGSKMOTLIEDVNTIEHFTVSCFPQPLEEC	120
QY	121	LREVOGNIISHLLKDYCTQTLALPKICGACONFSKCLEVOCCOPDSSSTLLPPSPALAEAT	180
Db	121	LREVOGNIISHLLKDYCTQTLALPKICGACONFSKCLEVOCCOPDSSSTLLPPSPALAEAT	180
QY	181	ELREPPRRQQLIIIIIIIEPLTVILAAAMGLRMQARRRGELHNGVLPDSHP	231
Db	181	ELREPPRRQQLIIIIIIIEPLTVILAAAMGLRMQARRRGELHNGVLPDSHP	231

## RESULT 4



```

US-10-095-449-6
Sequence 6, Application US/10095449
Patent No. US20020160004A1
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/095,449
FILING DATE: 13-Mar-2002
CLASSIFICATION: 350
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/669,692
FILING DATE: 24-JUN-1996
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TOPOLOGY: 1linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-095-449-6
Query Match 62.8% Score 768.5; DB 9; Length 235;
Best Local Similarity 70.3%; Pred. No. 6; 5e-65;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4
QY 1 MTVALPAWSPNSLLLLLLLSPCLRGTPDCYFSSPISSNFKVKPRLDTDLKDYPT 60
DB 1 MTVALPAWSP-TTYLLLLLLLLSSGLSGTODCSFQHSPISSDFAVKITRELSDYDLLQDYPT 59
QY 61 VAVNIODEKHCRAWLSLFLAQRWIEDLKTVAGSKMOTILEDVYTELTHFYTSCFQPLPQC 120
DB 60 VASNIODEELCGGLMRVLVAQKRMERLKTIVAGSKMGLERVATETLHYTKCAFQPPSC 119
QY 121 LRFVQTNIEHLKDTQTDLALPCIGKACONFSRCLVEQOCOPDSSSTLLPSPRIALEAT 180
DB 120 LRFVQTNIRLQETSEQVLAKPWITR--QNSRCLLEQOCQPDSSSTLPPSPRIALEAT 177
QY 181 ELPEPPRRQLLLLLLPLTVLVAAGLIRWQARRR----GELHPGVLP 228
DB 178 APTAPQPP--LTLTLPLVGLLVAAGLHMQRTRKTRPRDEQVPPVSP 227

```

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

? APPLICATION NUMBER: 08/066,354  
? FILING DATE: MAY 24, 1993  
?  
? ATTORNEY/AGENT INFORMATION:  
?  
? NAME: Malaska, Stephen L.  
? REGISTRATION NUMBER: 32,655  
? REFERENCE/DOCCKET NUMBER: 2813-  
? TELECOMMUNICATION INFORMATION:  
? TELEPHONE: (206) 587-0430  
? FAX: (206) 233-0644  
? TELETYPE: 756822  
?  
? INFORMATION FOR SEQ ID NO: 6:  
?  
? SEQUENCE CHARACTERISTICS:  
? LENGTH: 235 amino acids  
? TYPE: amino acid  
? TOPOLOGY: linear  
?  
? MOLECULE TYPE: protein  
?  
? SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
? IS-09-983-806-6

Query Match	62.88;	Score 766.5;	DB 10;	Length 235;
Best Local Similarity	70.38;	Pred. No. 6.5e-65;		
Matches 163;	Conservative 17;	Mismatches 43;	Indels 9;	Gaps 4;

[illegible]

```

RESULT 7
US-09-904-536-1
; Sequence 1, Application US/09904536
; Patent No. US20020111475A1
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03360, 0028
CURRENT APPLICATION NUMBER: US/09/904,536
PRIOR FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO. 1
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-904-536-1

```

Query Match	62.88;	Score 768.5;	DB 10;	Length 235;
Best Local Similarity	70.38;	Pred. No. 6.5e-65;		
Matches 163; Conservative	17;	Mismatches 43;	Indels 9;	Gaps 4;

[illegible]

QY 121 LRFVOTNLSHLKEDPCQLAKPKIGACGAFNSCGLCEVOOCOPSSLLPRSPRLAEAT 160  
| | | | | | | | | | | | | | | | | | | | | | | |  
Db 120 LRFVOTNLSRLDGEISBDLVAKPWIR-- QNFSCLELQCQPSPSTLPDPWSPRLAEAT 177  
| | | | | | | | | | | | | | | | | | | | | | | |  
QY 181 ELIPERPROULLILLPLVLVLAAMGLRWQRARR---GELHGVPLP 228  
| | | | | | | | | | | | | | | | | | | | | | | |  
Db 178 APTAAQPP--LILLELLIVGLILLAAAMCHMORTRRTERPGQVPVSP 227

RESULT 8  
 US-09-904-536-19  
 : Sequence 19, Application US/09904536  
 : Patent No. US2002011475A1  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Graddis, Thomas J.  
 : APPLICANT: McGrew, Jeffrey T.  
 : TITLE OF INVENTION: FL3-L MUTANTS AND METHODS OF USE  
 : FILE REFERENCE: 03260.0028  
 : CURRENT APPLICATION NUMBER: US/09/904,536  
 : PRIOR FILING DATE: 2001-07-16  
 : PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100  
 : NUMBER OF SEQ. ID NOS: 20  
 : SOFTWARE: PatentIn Ver. 2.1  
 :  
 : SEQ ID NO 19  
 : LENGTH: 137  
 :  
 : TYPE: PRT  
 : ORGANISM: Murine  
 :  
 : US-09-904-536-19

Query Match	59.28;	Score 724.5;	DB 10;	Length 137;
Best Local Similarity	99.38;	Pred. No. 4.3e-61;		
Matches 136; Conservative	0;	Mismatches 0;	Indels 1;	Gaps 1;

QY	28	TPRCYSHSPISNNKVFREITLHKDQVYVAVLQD-EKHCALMSLELQWRTEQ	86
Db	1	TPRCYSHSPISNNKVFREITDLHKDQVYVAVNLQDEEHCALMSLEFLQWRTEQ	60
QY	87	LKTVASKKQOTLEEDVNEHFVYSCFPPPLPESCLRVQTNINSHLKDTCYQLALPKCI	146
Db	61	LKTVASKKQOTLEEDVNEHFVYSCFPPPLPESCLRVQTNINSHLKDTCYQLALPKCI	120
QY	147	GKACQNFSSRCLEVQCAP	163
Db	121	GKACQNFSSRCLEVQCAP	137

```

RESULT 9
US-09-904-536-10
: Sequence 10, Application US/09904536
: Patent No. US20020111475A1
:
GENERAL INFORMATION:
: APPLICANT: Graddis, Thomas J.
: APPLICANT: McGrew, Jeffrey T.
: TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
: FILE REFERENCE: 03260, 0028
: CURRENT APPLICATION NUMBER: US/09/904,536
: CURRENT FILING DATE: 2001-07-16
: PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
: PRIOR FILING DATE: 1999-07-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 10
:
LENGTH: 212
:
TYPE: PRT
:
ORGANISM: Homo sapiens
:
US-09-904-536-10

```

Query Match	56.6%;	Score 692;	DB 10;	Length 212;
Best Local Similarity	69.9%;	Pred. No. 8.5e-58;		
Matches 144;	Conservative 15;	Mismatches 39;	Indels 8;	Gaps 3;

27 GTPDCYFESHSPISNFKVKFRELTDLKDYPTVAVNLDQDEKHCKALWSLFLAQRWIEQ 86

[illegible]

```

; SEQ_ID NO 14
;
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-14

Query Match          56.1%; Score 686; DB 10; Length 209;
Best Local Similarity 69.8%; Pred. No. 3e-57;
Matches 143; Conservative 15; Mismatches 39; Indels 8; Gaps 3;

QY      28  TPDCYFESHSPSSNFKVRFELTDLLKDYPTVAVNLQDEHKCAKMSLPLAQRWIRQL 87
Db      1  TQDCGFQHSPLSSDRAVKIRELSTDLQDPYPTVASNLQDEBLCGLMLVLAQRMMERL 60

QY      88  KTVASSKMQTLLEEDNTELIHEVTSCTFQPLRPCLRFVQVINISHLKDKYCTQALLAKPCIG 147
Db      61  KTVASSKMQGLLERNTETLIHEVTECAQFPSPCLRFVQVINISRLQETSEGLVALKAPIT 120

QY      148 KACQNFSRCLEVQCCPDSDSTLLPPRSPLALENTTELPEPRRQGLLLLLLLPLTVLLAA 207
Db      121 R--QNFSCRLELQCCPDSDSTLPPMSPRLPEATATPAQPp--LTLTLTLPLVGLLLAA 176

QY      208 WGLRWQRARR-----GELHPGVLP 228
Db      177 WCLHWQRTARRRRPRGEOVPPVPS 201

```

```

RESULT 12
US-09-904-536-18
; Sequence 18, Application US/09904536
; Patent No. US20020111475A1
; GENERAL INFORMATION:
; APPLICANT: McGraw, Thomas J.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904.536
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 209
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-904-536-18

Query Match          56.1%; Score 686; DB 10; Length 209;
Best Local Similarity 69.8%; Pred. No. 3e-57;
Matches 143; Conservative 15; Mismatches 39; Indels 8; Gaps 3;

QY      28  TPDQYSHSPSSINFRKVRRELTDHLMDYPTVAVNIODEKHCKALMSFLAQRWIEQL 87
      1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1  TQDCSFQHSPISSIDPAVKYIRELSIDYLDQDPYTVASNIQDEELCGIMRWLYLAQRMERL 60
      1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      88  KTVASSKMOITLEDVNTLHFTVTSCTPQRLPRLCLRFVQNTISHLKDKPTOTLAKPCIG 147
      1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61  KTVASSKMOGLIERNTLHFTVTKCAFPQPSCLRFVQNTISRLQETSEQLVALKPWIT 120
      1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      148  KACQNFSRCLFVOCOPDSSTLLPPRSPLALEATELPEPRPROLLLLLLPLTVLAAA 207
      1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      121  R--QNFSRCLFVOCOPDSSTLLPPRMSPRLENTAPTAQPP--LLLLLLPLVGLLLAAA 176
      1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      208  WGLRWQARARR--GELHPGVLP 228
      1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      177  WCLHMQRTRRRPRRPGEQVPVPSP 201
      1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 13
US-09-904-536-16
; Sequence 16, Application US/09904536
; Patent No. US20020111475A1

```

```
; GENERAL INFORMATION:
; APPLICANT: Gradadis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-16

Query Match          56.0%; Score 685; DB 10; Length 209;
Best Local Similarity 69.3%; Pred. No. 3.8e-57;
Matches 143; Conservative 15; Mismatches 39; Indels 8; Gaps 3;

OY 28 TPDGFSHPISSNFKVKFRELTDHLKDYPTVAVNLQDEKHKALMSFLAQRTEQL 87
DB 1 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTASNLODEELCGGLMRLVLAQRMMERL 60
OY 88 KTVAGSKMQTLLEDVNTIEHFVTSCTFQPLPECLRFVQTNISHLKDTCTQLALPKPCIG 147
DB 61 KTVAGSKMQGLLEVRNTEIHFVTKCAFPQPPSCLRFVQTNISRLQETSQVALKPWIT 120
OY 148 KACONFSRCLEVOQOPDSSSTLLPPRSPIALEATELPEPRRQLLLLLLPLTVLAAA 207
DB 121 R--QNFSCRLELOQOPDSSSTLLPPWSRPLEATAPTAQP--LTLILLPLVGLLLAAA 176
OY 208 WGLRMQARRR---GELHGPVLP 228
DB 177 WCLHMQTRRRTPRPGQVPPVPS 201

RESULT 14
US-09-904-536-9
; Sequence 9, Application US/09904536
; Patent No. US2002011475A1
; GENERAL INFORMATION:
; APPLICANT: Gradadis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-9

Query Match          55.8%; Score 682; DB 10; Length 209;
Best Local Similarity 69.3%; Pred. No. 7.2e-57;
Matches 142; Conservative 15; Mismatches 40; Indels 8; Gaps 3;

OY 28 TPDGFSHPISSNFKVKFRELTDHLKDYPTVAVNLQDEKHKALMSFLAQRTEQL 87
DB 1 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTASNLODEELCGGLMRLVLAQRMMERL 60
OY 88 KTVAGSKMQTLLEDVNTIEHFVTSCTFQPLPECLRFVQTNISHLKDTCTQLALPKPCIG 147
DB 61 KTVAGSKMQGLLEVRNTEIHFVTKCAFPQPPSCLRFVQTNISRLQETSQVALKPWIT 120
OY 148 KACONFSRCLEVOQOPDSSSTLLPPRSPIALEATELPEPRRQLLLLLLPLTVLAAA 207
DB 121 R--QNFSCRLELOQOPDSSSTLLPPWSRPLEATAPTAQP--LTLILLPLVGLLLAAA 176
OY 208 WGLRMQARRR---GELHGPVLP 228
DB 177 WCLHMQTRRRTPRPGQVPPVPS 201

US-09-904-536-9
```

```
DB 121 R--QNFSCRLELOQOPDSSSTLLPPWSRPLEATAPTAQP--LTLILLPLVGLLLAAA 176
OY 208 WGLRMQARRR---GELHGPVLP 228
DB 177 WCLHMQTRRRTPRPGQVPPVPS 201

RESULT 15
US-09-904-536-12
; Sequence 12, Application US/09904536
; Patent No. US2002011475A1
; GENERAL INFORMATION:
; APPLICANT: Gradadis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-12

Query Match          55.8%; Score 682; DB 10; Length 209;
Best Local Similarity 69.3%; Pred. No. 7.2e-57;
Matches 142; Conservative 15; Mismatches 40; Indels 8; Gaps 3;

OY 28 TPDGFSHPISSNFKVKFRELTDHLKDYPTVAVNLQDEKHKALMSFLAQRTEQL 87
DB 1 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTASNLODEELCGGLMRLVLAQRMMERL 60
OY 88 KTVAGSKMQTLLEDVNTIEHFVTSCTFQPLPECLRFVQTNISHLKDTCTQLALPKPCIG 147
DB 61 KTVAGSKMQGLLEVRNTEIHFVTKCAFPQPPSCLRFVQTNISRLQETSQVALKPWIT 120
OY 148 KACONFSRCLEVOQOPDSSSTLLPPRSPIALEATELPEPRRQLLLLLLPLTVLAAA 207
DB 121 R--QNFSCRLELOQOPDSSSTLLPPWSRPLEATAPTAQP--LTLILLPLVGLLLAAA 176
OY 208 WGLRMQARRR---GELHGPVLP 228
DB 177 WCLHMQTRRRTPRPGQVPPVPS 201
```

Search completed: November 24, 2002, 10:18:12  
Job time : 9.42704 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 24, 2002, 10:10:16 ; Search time 135.328 Seconds  
(without alignments)  
1100.533 Million cell updates/sec

Title: US-09-448-378-2  
1223  
Perfect score: 1223  
Sequence: 1 MVLAPAWSPNSILLILL.....WQARRRGELHPGVLPSPHP 231

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 64473110 residues  
Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Pending\_Patents\_AA\_Main:\*

- 1: /cgn2\_6/ptodata/1/paa/PCRTQS\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/paa/US06\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/paa/US07\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/paa/US08\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/paa/US081\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/paa/US082\_COMB.pep.\*
- 7: /cgn2\_6/ptodata/1/paa/US083\_COMB.pep.\*
- 8: /cgn2\_6/ptodata/1/paa/US084\_COMB.pep.\*
- 9: /cgn2\_6/ptodata/1/paa/US085\_COMB.pep.\*
- 10: /cgn2\_6/ptodata/1/paa/US086\_COMB.pep.\*
- 11: /cgn2\_6/ptodata/1/paa/US087\_COMB.pep.\*
- 12: /cgn2\_6/ptodata/1/paa/US088\_COMB.pep.\*
- 13: /cgn2\_6/ptodata/1/paa/US089\_COMB.pep.\*
- 14: /cgn2\_6/ptodata/1/paa/US090\_COMB.pep.\*
- 15: /cgn2\_6/ptodata/1/paa/US091\_COMB.pep.\*
- 16: /cgn2\_6/ptodata/1/paa/US092\_COMB.pep.\*
- 17: /cgn2\_6/ptodata/1/paa/US093\_COMB.pep.\*
- 18: /cgn2\_6/ptodata/1/paa/US094\_COMB.pep.\*
- 19: /cgn2\_6/ptodata/1/paa/US095\_COMB.pep.\*
- 20: /cgn2\_6/ptodata/1/paa/US096\_COMB.pep.\*
- 21: /cgn2\_6/ptodata/1/paa/US097\_COMB.pep.\*
- 22: /cgn2\_6/ptodata/1/paa/US098\_COMB.pep.\*
- 23: /cgn2\_6/ptodata/1/paa/US099\_COMB.pep.\*
- 24: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep.\*
- 25: /cgn2\_6/ptodata/1/paa/US101\_COMB.pep.\*
- 26: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep.\*
- 27: /cgn2\_6/ptodata/1/paa/US60\_COMB.pep.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1223	100.0	231	PCT-US98-12085-2	Sequence 2, Appl
2	1223	100.0	231	US-08-068-394-2	Sequence 2, Appl
3	1223	100.0	231	US-08-106-463-2	Sequence 2, Appl
4	1223	100.0	231	US-08-111-758-2	Sequence 2, Appl
5	1223	100.0	231	US-08-162-407-2	Sequence 2, Appl
6	1223	100.0	231	US-08-444-625-2	Sequence 2, Appl

7	1223	100.0	231	US-08-444-626-2	Sequence 2, Appl
8	1223	100.0	231	US-08-444-632-2	Sequence 2, Appl
9	1223	100.0	231	US-08-669-692-2	Sequence 2, Appl
10	1223	100.0	231	US-08-877-421-2	Sequence 2, Appl
11	1223	100.0	231	US-08-448-378-2	Sequence 2, Appl
12	1223	100.0	231	US-09-629-430B-8	Sequence 8, Appl
13	1223	100.0	231	US-09-983-806-2	Sequence 2, Appl
14	1223	100.0	231	US-10-095-449-2	Sequence 2, Appl
15	1223	100.0	231	US-60-368-263-2	Sequence 2, Appl
16	1212.5	99.1	232	US-08-155-111-38	Sequence 38, Appl
17	1212.5	99.1	232	US-08-162-413-38	Sequence 38, Appl
18	1212.5	99.1	232	US-08-261-553-38	Sequence 38, Appl
19	1212.5	99.1	232	US-08-472-168-38	Sequence 38, Appl
20	1212.5	99.1	232	US-08-484-882-38	Sequence 38, Appl
21	1212.5	99.1	232	US-08-486-661-38	Sequence 38, Appl
22	1212.5	99.1	232	US-09-791-537-86787	Sequence 86787, A
23	1212.5	99.1	232	US-09-629-430B-13	Sequence 13, Appl
24	1208.5	98.8	232	US-09-791-537-51625	Sequence 51625, A
25	1208.5	98.8	232	US-09-791-537-51625	Sequence 25, Appl
26	1006	82.3	287	US-09-501-097A-25	Sequence 25, Appl
27	1004	82.1	189	PCT-US02-08033-18	Sequence 18, Appl
28	1004	82.1	189	US-09-629-430B-9	Sequence 9, Appl
29	1004	82.1	289	PCT-US02-08033-20	Sequence 20, Appl
30	879	71.9	172	US-09-629-430B-17	Sequence 17, Appl
31	879	71.9	172	US-09-791-537-18574	Sequence 18574, A
32	879	71.9	220	US-09-629-430B-11	Sequence 11, Appl
33	879	71.9	220	US-09-629-430B-15	Sequence 15, Appl
34	874	71.5	169	US-09-791-537-122072	Sequence 122072, A
35	774	63.3	294	US-09-322-409-7	Sequence 7, Appl
36	774	63.3	294	US-09-451-527-7	Sequence 7, Appl
37	774	63.3	294	US-10-218-654-7	Sequence 7, Appl
38	774	63.3	294	US-10-262-439-7	Sequence 7, Appl
39	772.5	63.2	235	US-08-155-111-34	Sequence 34, Appl
40	772.5	63.2	235	US-08-162-413-34	Sequence 34, Appl
41	772.5	63.2	235	US-08-261-553-34	Sequence 34, Appl
42	772.5	63.2	235	US-08-472-168-34	Sequence 34, Appl
43	772.5	63.2	235	US-08-484-882-34	Sequence 34, Appl
44	772.5	63.2	235	US-08-486-661-34	Sequence 34, Appl
45	772.5	63.2	235	US-09-629-430B-23	Sequence 23, Appl

#### ALIGNMENTS

RESULT 1  
PCT-US98-12085-2  
Sequence 2, Application PC/US9812085  
GENERAL INFORMATION:  
APPLICANT: IMMUNEX CORPORATION  
TITLE OF INVENTION: A Method of Enhancing Antigen-Specific Peripheral Immune To  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM/PC Compatible  
OPERATING SYSTEM: MS-DOS/Windows 95  
SOFTWARE: Word for Windows 95, Version 7.0a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US98/12085  
FILING DATE: 12-JUN-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2855-WO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 231 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US98-12085-2

Query Match 100.0%; Score 1223; DB 1; Length 231;  
Best Local Similarity 100.0%; Pred. No. 3.5e-110;  
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLLILLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLKDYPT 60  
Db 1 MTVLAPAMSPNSLLILLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLKDYPT 60  
QY 61 VAVNLQDEKCKALMSFLAQRWIEQLKTVAGSKMOTLLEDVNTETIHVTSCTFQPLPEC 120  
Db 61 VAVNLQDEKCKALMSFLAQRWIEQLKTVAGSKMOTLLEDVNTETIHVTSCTFQPLPEC 120  
QY 121 LRFVQTNISHLKDTCTQLALPKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPIALEAT 180  
Db 121 LRFVQTNISHLKDTCTQLALPKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPIALEAT 180  
QY 181 ELPEPRPQQLLLLLPLTLVLLAAAGLRFWRARRRGEIHPGVLPSPHP 231  
Db 181 ELPEPRPQQLLLLLPLTLVLLAAAGLRFWRARRRGEIHPGVLPSPHP 231

RESULT 2  
US-08-068-394-2  
Sequence 2, Application US/08068394  
GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.  
APPLICANT: Beckmann, M. Patricia  
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/068,394  
FILING DATE: 19930524  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2813  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 231 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-068-394-2

Query Match 100.0%; Score 1223; DB 4; Length 231;  
Best Local Similarity 100.0%; Pred. No. 3.5e-110;

Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLLILLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLKDYPT 60  
Db 1 MTVLAPAMSPNSLLILLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLKDYPT 60  
QY 61 VAVNLQDEKCKALMSFLAQRWIEQLKTVAGSKMOTLLEDVNTETIHVTSCTFQPLPEC 120  
Db 61 VAVNLQDEKCKALMSFLAQRWIEQLKTVAGSKMOTLLEDVNTETIHVTSCTFQPLPEC 120  
QY 121 LRFVQTNISHLKDTCTQLALPKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPIALEAT 180  
Db 121 LRFVQTNISHLKDTCTQLALPKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPIALEAT 180  
QY 181 ELPEPRPQQLLLLLPLTLVLLAAAGLRFWRARRRGEIHPGVLPSPHP 231  
Db 181 ELPEPRPQQLLLLLPLTLVLLAAAGLRFWRARRRGEIHPGVLPSPHP 231

RESULT 3  
US-08-106-463-2  
Sequence 2, Application US/08106463  
GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.  
APPLICANT: Beckmann, M. Patricia  
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/106,463  
FILING DATE: 19930812  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2813-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 231 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-106-463-2

Query Match 100.0%; Score 1223; DB 5; Length 231;  
Best Local Similarity 100.0%; Pred. No. 3.5e-110;  
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLLILLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLKDYPT 60  
Db 1 MTVLAPAMSPNSLLILLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLKDYPT 60  
QY 61 VAVNLQDEKCKALMSFLAQRWIEQLKTVAGSKMOTLLEDVNTETIHVTSCTFQPLPEC 120  
Db 61 VAVNLQDEKCKALMSFLAQRWIEQLKTVAGSKMOTLLEDVNTETIHVTSCTFQPLPEC 120  
QY 121 LRFVQTNISHLKDTCTQLALPKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPIALEAT 180  
Db 121 LRFVQTNISHLKDTCTQLALPKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPIALEAT 180

Db 121 LRFVQTNISHLKDKTCQTOLALKPCIGKACONFSRCLEVOQCPDSSSTLLPPRSPALAEAT 180  
QY 181 ELPEPRRQLLLLLLPLTLVLLAAAGLRRQARRRGGELHGPVLPSPH 231  
Db 181 ELPEPRRQLLLLLLPLTLVLLAAAGLRRQARRRGGELHGPVLPSPH 231

## RESULT 4

US-08-111-758-2  
Sequence 2, Application US/08111758  
GENERAL INFORMATION:  
APPLICANT: Lyman, Stewart D.  
APPLICANT: Beckmann, M. Patricia  
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.0.1  
SOFTWARE: Microsoft Word, Version #5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/111,758  
FILING DATE: August 25, 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/106,463  
FILING DATE: August 12, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/068,394  
FILING DATE: May 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2813-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 231 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-111-758-2

Query Match 100.0%; Score 1223; DB 5; Length 231;  
Best Local Similarity 100.0%; Pred. No. 3.5e-110; Indels 0; Gaps 0;  
Matches 231; Conservative 0; Mismatches 0;

QY 1 MTVLAPAMSPNSLLLLLSPLCRGTPDCYFSHPISSNFKYKFRLETDHLKDYPT 60  
Db 1 MTVLAPAMSPNSLLLLLSPLCRGTPDCYFSHPISSNFKYKFRLETDHLKDYPT 60  
QY 61 VAVNLQDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120  
Db 61 VAVNLQDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120  
QY 121 LRFVQTNISHLKDKTCQTOLALKPCIGKACONFSRCLEVOQCPDSSSTLLPPRSPALAEAT 180  
Db 121 LRFVQTNISHLKDKTCQTOLALKPCIGKACONFSRCLEVOQCPDSSSTLLPPRSPALAEAT 180  
QY 181 ELPEPRRQLLLLLLPLTLVLLAAAGLRRQARRRGGELHGPVLPSPH 231  
Db 181 ELPEPRRQLLLLLLPLTLVLLAAAGLRRQARRRGGELHGPVLPSPH 231

RESULT 5  
US-08-162-407-2  
Sequence 2, Application US/08162407  
GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.  
APPLICANT: Beckmann, M. Patricia  
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.0.1  
SOFTWARE: Microsoft Word, Version #5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,407  
FILING DATE: December 3, 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/111,758  
FILING DATE: August 25, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/106,463  
FILING DATE: August 12, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/068,394  
FILING DATE: May 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2813-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 231 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-162-407-2

Query Match 100.0%; Score 1223; DB 5; Length 231;  
Best Local Similarity 100.0%; Pred. No. 3.5e-110; Indels 0; Gaps 0;  
Matches 231; Conservative 0; Mismatches 0;

QY 1 MTVLAPAMSPNSLLLLLSPLCRGTPDCYFSHPISSNFKYKFRLETDHLKDYPT 60  
Db 1 MTVLAPAMSPNSLLLLLSPLCRGTPDCYFSHPISSNFKYKFRLETDHLKDYPT 60  
QY 61 VAVNLQDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120  
Db 61 VAVNLQDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120  
QY 121 LRFVQTNISHLKDKTCQTOLALKPCIGKACONFSRCLEVOQCPDSSSTLLPPRSPALAEAT 180  
Db 121 LRFVQTNISHLKDKTCQTOLALKPCIGKACONFSRCLEVOQCPDSSSTLLPPRSPALAEAT 180  
QY 181 ELPEPRRQLLLLLLPLTLVLLAAAGLRRQARRRGGELHGPVLPSPH 231  
Db 181 ELPEPRRQLLLLLLPLTLVLLAAAGLRRQARRRGGELHGPVLPSPH 231

RESULT 6  
US-08-444-625-2

```
? Sequence 2, Application US/08444625
? GENERAL INFORMATION:
? APPLICANT: Lyman, Stewart D.
? APPLICANT: Beckmann, M. Patricia
? TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Stephen L. Malaska, Immunex Corporation
? STREET: 51 University Street
? CITY: Seattle
? STATE: Washington
? COUNTRY: US
? ZIP: 98101
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: Apple Macintosh
? OPERATING SYSTEM: Macintosh 7.0.1
? SOFTWARE: Microsoft Word, Version #5.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/444,625
? CLASSIFICATION: 424
? FILING DATE: 19-MAY-1995
? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER: US 08/162,407
? FILING DATE: 03-DEC-1993
? APPLICATION NUMBER: 08/111,758
? FILING DATE: August 25, 1993
? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER: 08/106,463
? FILING DATE: August 12, 1993
? CLASSIFICATION: 424
? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER: 08/068,394
? FILING DATE: May 24, 1993
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: Malaska, Stephen L.
? REGISTRATION NUMBER: 32,655
? REFERENCE/DOCKET NUMBER: 2813-C
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (206) 587-0430
? TELEFAX: (206) 233-0644
? TELEX: 756822
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 231 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-08-444-625-2
```

```
Query Match 100.0%; Score 1223; DB 8; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.5e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLSLILLLISPCLRGTPDCYFSHSPISNNKVKVFRRLTDHLKDYPVT 60
DB 1 MTVLAPAMSPNSLSLILLLISPCLRGTPDCYFSHSPISNNKVKVFRRLTDHLKDYPVT 60
QY 61 VAVNLQDEKHKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTLHFVTSCTFPQPLEC 120
DB 61 VAVNLQDEKHKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTLHFVTSCTFPQPLEC 120
QY 121 LRFVQTNISHLKDTQTQLALKPCIGKACQNFSCRLEVOQCPDSSSTLLPPRSPIALEAT 180
DB 121 LRFVQTNISHLKDTQTQLALKPCIGKACQNFSCRLEVOQCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQULLLLPLTLVLAAAGLRLWQARRRGEHLHPGVLPDPSHP 231
DB 181 ELPEPRRQULLLLPLTLVLAAAGLRLWQARRRGEHLHPGVLPDPSHP 231
```

RESULT 7

```
US-08-444-626-2
? Sequence 2, Application US/08444626
? GENERAL INFORMATION:
? APPLICANT: Lyman, Stewart D.
? APPLICANT: Beckmann, M. Patricia
? TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Stephen L. Malaska, Immunex Corporation
? STREET: 51 University Street
? CITY: Seattle
? STATE: Washington
? COUNTRY: US
? ZIP: 98101
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: Apple Macintosh
? OPERATING SYSTEM: Macintosh 7.0.1
? SOFTWARE: Microsoft Word, Version #5.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/444,626
? CLASSIFICATION: 530
? FILING DATE: 19-MAY-1995
? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER: US 08/162,407
? FILING DATE: 03-DEC-1993
? APPLICATION NUMBER: 08/111,758
? FILING DATE: August 25, 1993
? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER: 08/106,463
? FILING DATE: August 12, 1993
? CLASSIFICATION: 530
? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER: 08/068,394
? FILING DATE: May 24, 1993
? CLASSIFICATION: 530
? ATTORNEY/AGENT INFORMATION:
? NAME: Malaska, Stephen L.
? REGISTRATION NUMBER: 32,655
? REFERENCE/DOCKET NUMBER: 2813-C
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (206) 587-0430
? TELEFAX: (206) 233-0644
? TELEX: 756822
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 231 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-08-444-626-2
```

```
Query Match 100.0%; Score 1223; DB 8; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.5e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLSLILLLISPCLRGTPDCYFSHSPISNNKVKVFRRLTDHLKDYPVT 60
DB 1 MTVLAPAMSPNSLSLILLLISPCLRGTPDCYFSHSPISNNKVKVFRRLTDHLKDYPVT 60
QY 61 VAVNLQDEKHKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTLHFVTSCTFPQPLEC 120
DB 61 VAVNLQDEKHKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTLHFVTSCTFPQPLEC 120
QY 121 LRFVQTNISHLKDTQTQLALKPCIGKACQNFSCRLEVOQCPDSSSTLLPPRSPIALEAT 180
DB 121 LRFVQTNISHLKDTQTQLALKPCIGKACQNFSCRLEVOQCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQULLLLPLTLVLAAAGLRLWQARRRGEHLHPGVLPDPSHP 231
DB 181 ELPEPRRQULLLLPLTLVLAAAGLRLWQARRRGEHLHPGVLPDPSHP 231
```



```
RESULT 8
US-08-444-632-2
; Sequence 2, Application US/08444632
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,632
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-444-632-2

Query Match 100.0%; Score 1223; DB 8; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.5e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 9
US-08-669-692-2
; Sequence 2, Application US/08669692
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,692
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-669-692-2

Query Match 100.0%; Score 1223; DB 10; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.5e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 10
US-08-877-421-2
; Sequence 2, Application US/08877421
; GENERAL INFORMATION:
; APPLICANT: Viney, Joanne L.
; APPLICANT: Mowatt, Allan M.
; APPLICANT: Abbott, Nicholas
; TITLE OF INVENTION: A Method of Enhancing Antigen-Specific Peripheral Immune Tol
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Macintosh 7.6
; SOFTWARE: Microsoft Word, Version #6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,421
; FILING DATE: 17-JUN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2855
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-877-421-2

Query Match      100.0%; Score 1223; DB 12; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.5e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPNSLLILLSPCLRGTPDCYFSHSPISSNKVKFRELTHLKDYPVT 60
D 1 MTVALPAMSPNSLLILLSPCLRGTPDCYFSHSPISSNKVKFRELTHLKDYPVT 60
QY 61 VAVNLDEKCKALMSLFLAQRWIEDLKTIVAGSKMOTILEDVNTLHFTVSTCFQPLPEC 120
D 61 VAVNLDEKCKALMSLFLAQRWIEDLKTIVAGSKMOTILEDVNTLHFTVSTCFQPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLALPKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPALBAT 180
D 121 LRFVQTNISHLKDTCTQLALPKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPALBAT 180
QY 181 ELPEPRRQRLILLPLTLVLLAAWGLRMQRRARRGELHPGVLPSP 231
D 181 ELPEPRRQRLILLPLTLVLLAAWGLRMQRRARRGELHPGVLPSP 231

RESULT 11
US-09-448-378-2
; Sequence 2, Application US/09448378
; GENERAL INFORMATION:
; APPLICANT: Brasel, Kenneth
; TITLE OF INVENTION: Dendritic Cell Stimulatory Factor
; FILE REFERENCE: 2836-D
; CURRENT APPLICATION NUMBER: US/09/448,378
; CURRENT FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 2
```

```
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-448-378-2

Query Match      100.0%; Score 1223; DB 18; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.5e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPNSLLILLSPCLRGTPDCYFSHSPISSNKVKFRELTHLKDYPVT 60
D 1 MTVALPAMSPNSLLILLSPCLRGTPDCYFSHSPISSNKVKFRELTHLKDYPVT 60
QY 61 VAVNLDEKCKALMSLFLAQRWIEDLKTIVAGSKMOTILEDVNTLHFTVSTCFQPLPEC 120
D 61 VAVNLDEKCKALMSLFLAQRWIEDLKTIVAGSKMOTILEDVNTLHFTVSTCFQPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLALPKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPALBAT 180
D 121 LRFVQTNISHLKDTCTQLALPKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPALBAT 180
QY 181 ELPEPRRQRLILLPLTLVLLAAWGLRMQRRARRGELHPGVLPSP 231
D 181 ELPEPRRQRLILLPLTLVLLAAWGLRMQRRARRGELHPGVLPSP 231

RESULT 12
US-09-629-430B-8
; Sequence 8 Application US/09629430B
; GENERAL INFORMATION:
; APPLICANT: Hermanson, Gary George
; TITLE OF INVENTION: FLT-3-Ligand-Encoding Polynucleotide as a
; FILE REFERENCE: 1530.0130001
; CURRENT APPLICATION NUMBER: US/09/629,430B
; CURRENT FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 60/146,170
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-629-430B-8

Query Match      100.0%; Score 1223; DB 20; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.5e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPNSLLILLSPCLRGTPDCYFSHSPISSNKVKFRELTHLKDYPVT 60
D 1 MTVALPAMSPNSLLILLSPCLRGTPDCYFSHSPISSNKVKFRELTHLKDYPVT 60
QY 61 VAVNLDEKCKALMSLFLAQRWIEDLKTIVAGSKMOTILEDVNTLHFTVSTCFQPLPEC 120
D 61 VAVNLDEKCKALMSLFLAQRWIEDLKTIVAGSKMOTILEDVNTLHFTVSTCFQPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLALPKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPALBAT 180
D 121 LRFVQTNISHLKDTCTQLALPKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPALBAT 180
QY 181 ELPEPRRQRLILLPLTLVLLAAWGLRMQRRARRGELHPGVLPSP 231
D 181 ELPEPRRQRLILLPLTLVLLAAWGLRMQRRARRGELHPGVLPSP 231

RESULT 13
US-09-983-806-2
; Sequence 2, Application US/09983806
; GENERAL INFORMATION:
```

APPLICANT: Lyman, Stewart D.  
Beckmann, M. Patricia  
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.0.1  
SOFTWARE: Microsoft Word, Version #5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/983,806  
FILING DATE: 25-Oct-2001  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/444,626  
FILING DATE: 19-MAY-1995  
APPLICATION NUMBER: US 08/162,407  
FILING DATE: 03-DEC-1993  
APPLICATION NUMBER: 08/111,758  
FILING DATE: August 25, 1993  
APPLICATION NUMBER: 08/106,463  
FILING DATE: August 12, 1993  
APPLICATION NUMBER: 08/068,394  
FILING DATE: May 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2813-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 231 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-983-806-2  
Query Match 100.0%; Score 1223; DB 23; Length 231;  
Best Local Similarity 100.0%; Pred. No. 3.5e-110; Indels 0; Gaps 0;  
Matches 231; Conservative 0; Mismatches 0;  
QY 1 MTVLAPAMSPNSLLLLLLSPCLRGTPDCYFSHSPISNFKVRFRELDHLKDYPT 60  
DB 1 MTVLAPAMSPNSLLLLLLSPCLRGTPDCYFSHSPISNFKVRFRELDHLKDYPT 60  
QY 61 VAVNLODEKHCALMSLFLAQRWIEQLKTVAAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 120  
DB 61 VAVNLODEKHCALMSLFLAQRWIEQLKTVAAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 120  
QY 121 LRFVQNTINSHLKTCTQLALKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPALAEAT 180  
DB 121 LRFVQNTINSHLKTCTQLALKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPALAEAT 180  
QY 181 ELPEPRRQLLLLLLPLTLVLAAAGLIRWQARRRGELHGPVLPSPH 231  
DB 181 ELPEPRRQLLLLLLPLTLVLAAAGLIRWQARRRGELHGPVLPSPH 231  
RESULT 14  
US-10-095-449-2  
; Sequence 2, Application US/10095449  
; GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.  
Beckmann, M. Patricia  
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.0.1  
SOFTWARE: Microsoft Word, Version #5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/095,449  
FILING DATE: 13-Mar-2002  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/669,692  
FILING DATE: 24-JUN-1996  
APPLICATION NUMBER: US/08/162,407  
FILING DATE: December 3, 1993  
APPLICATION NUMBER: 08/111,758  
FILING DATE: August 25, 1993  
APPLICATION NUMBER: 08/106,463  
FILING DATE: August 12, 1993  
APPLICATION NUMBER: 08/068,394  
FILING DATE: May 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2813-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 231 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-095-449-2  
Query Match 100.0%; Score 1223; DB 24; Length 231;  
Best Local Similarity 100.0%; Pred. No. 3.5e-110; Indels 0; Gaps 0;  
Matches 231; Conservative 0; Mismatches 0;  
QY 1 MTVLAPAMSPNSLLLLLLSPCLRGTPDCYFSHSPISNFKVRFRELDHLKDYPT 60  
DB 1 MTVLAPAMSPNSLLLLLLSPCLRGTPDCYFSHSPISNFKVRFRELDHLKDYPT 60  
QY 61 VAVNLODEKHCALMSLFLAQRWIEQLKTVAAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 120  
DB 61 VAVNLODEKHCALMSLFLAQRWIEQLKTVAAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 120  
QY 121 LRFVQNTINSHLKTCTQLALKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPALAEAT 180  
DB 121 LRFVQNTINSHLKTCTQLALKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPALAEAT 180  
QY 181 ELPEPRRQLLLLLLPLTLVLAAAGLIRWQARRRGELHGPVLPSPH 231  
DB 181 ELPEPRRQLLLLLLPLTLVLAAAGLIRWQARRRGELHGPVLPSPH 231  
RESULT 15  
US-60-368-263-2  
; Sequence 2, Application US/60368263  
; GENERAL INFORMATION:

```
; APPLICANT: McKenna, Hilary J.  
; APPLICANT: Liebowitz, David N.  
; APPLICANT: Maliszewski, Charles R.  
; TITLE OF INVENTION: METHODS OF USING FLT-3 LIGAND IN IMMUNIZATION PROTOCOLS  
; FILE REFERENCE: 3399  
; CURRENT APPLICATION NUMBER: US/60/368,263  
; CURRENT FILING DATE: 2002-03-26  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 231  
; TYPE: PRT  
; ORGANISM: Mus sp  
; US-60-368-263-2
```

```
Query Match 100.0%; Score 1223; DB 27; Length 231;  
Best Local Similarity 100.0%; Pred. No. 3.5e-110;  
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MTVLAPAMSPNSILLILLLLSPCLRGTPDCYFSHSPISSNFKYKPRELTDHLKDYPT 60  
Db 1 MTVLAPAMSPNSILLILLLLSPCLRGTPDCYFSHSPISSNFKYKPRELTDHLKDYPT 60  
QY 61 VAVNLDEKCKALMSLFLAQRWIEQLKYAGSKMOTLLEDVNTETIHFTVSTCFQPLPEC 120  
Db 61 VAVNLDEKCKALMSLFLAQRWIEQLKYAGSKMOTLLEDVNTETIHFTVSTCFQPLPEC 120  
QY 121 LRFVQNTISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDSTLLPPRSPIALEAT 180  
Db 121 LRFVQNTISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDSTLLPPRSPIALEAT 180  
QY 181 ELPEPRPRQLLLLLPLTLVLVLAAMGLRWQARRRGELHPCVPLPSHP 231  
Db 181 ELPEPRPRQLLLLLPLTLVLVLAAMGLRWQARRRGELHPCVPLPSHP 231
```

Search completed: November 24, 2002, 10:17:26  
Job time: 136.328 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 24, 2002, 10:08:46 ; Search time 14.6245 Seconds  
(without alignments)  
1544.781 Million cell updates/sec

Title: us-09-448-378-1

Perfect score: 1242

Sequence: 1 MTVLAPAWSPTTYLLLLLL.....RPGGVPPVSPQDLLLVH 235

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	235	2 I38440	flt3 ligand - huma
2	864.5	69.6	245	2 S43293	FLT3/FLK2 ligand (
3	834	67.1	178	2 I39076	flt3 ligand altern
4	768.5	61.9	231	2 A49265	flt3/FLK-2 ligand
5	606.5	48.8	220	2 S43291	FLT3/FLK2 ligand (
6	606.5	48.8	220	2 I58343	flt3 ligand isofor
7	93	7.5	1217	2 T22672	hypothetical prote
8	92	7.4	661	1 TNBE12	74K alpha trans-in
9	89.5	7.2	474	2 T19543	hypothetical prote
10	89	7.2	387	2 I48201	adhalin - golden h
11	89	7.2	793	2 S60735	splicing factor SF
12	88.5	7.1	238	2 AB1990	hypothetical prote
13	88.5	7.1	1386	2 T00257	hypothetical prote
14	88	7.1	753	2 J00532	OP protein - kenne
15	87.5	7.0	919	1 A32290	protein-tyrosine-p
16	87	7.0	910	2 A53137	tyrosine kinase re
17	86.5	7.0	590	2 A40437	glutamic acid-rich
18	86	6.9	299	2 T17832	hypothetical prote
19	86	6.9	485	2 A33647	sulfated surface p
20	86	6.9	746	2 T28004	hypothetical prote
21	85	6.8	289	2 A87646	hypothetical prote
22	85	6.8	366	2 A37374	Fc gamma (196) rec
23	84	6.8	263	2 T03162	tegment protein 6
24	84	6.8	757	2 A39283	gamma-glutamyl car
25	83.5	6.7	199	2 E75630	hypothetical prote
26	83.5	6.7	530	2 A45690	transactivator EBN
27	83	6.7	1509	2 T19486	hypothetical prote
28	82.5	6.6	418	2 T19800	hypothetical prote
29	82.5	6.6	426	2 I36948	Ig epsilon-chain -

30	82.5	6.6	512	2 D40829	activin receptor 1
31	82.5	6.6	513	2 J01484	proline/leucine-r1
32	82	6.6	106	2 T06479	hypothetical prote
33	82	6.6	854	2 T23837	hypothetical prote
34	81.5	6.6	485	2 C75460	stromelysin 3 (EC
35	81.5	6.6	488	2 S13423	hypothetical prote
36	81.5	6.6	958	2 T13593	related to cytoske
37	81.5	6.6	1119	2 T50995	cysteine-rich exte
38	81	6.5	196	2 B48232	hypothetical prote
39	81	6.5	209	2 A48232	probable transpos
40	81	6.5	294	2 A12016	Ig epsilon chain C
41	81	6.5	388	2 S15591	class I cytochrome
42	81	6.5	428	1 BHHU	hypothetical prote
43	80.5	6.5	636	2 JN0047	hypothetical prote
44	80.5	6.5	1176	2 T49482	hypothetical prote
45	80.5	6.5	1306	2 T13592	hypothetical prote

ALIGNMENTS

RESULT 1

I38440  
flt3 ligand - human  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 01-Dec-2000  
C:Accession: I38440; I39075; S43292  
R:Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Escobar, S.S.; Downe  
Blood 83, 2795-2801, 1994  
A:Title: Cloning of the human homologue of the murine flt3 ligand: a growth factor fo  
A:Reference number: I38440; MUID:94235842; PMID:8180375  
A:Accession: I38440  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-235 <RES>  
A:Cross-references: EMBL:U03858; NID:g494978; PIDN:AAA19825.1; PID:g494979  
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.  
Oncogene 11, 1165-1172, 1995  
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.  
A:Reference number: I39075; MUID:96032581; PMID:7565977  
A:Accession: I39075  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-235 <RES>  
A:Cross-references: EMBL:U029874; NID:g1072036; PIDN:AAA90949.1; PID:g1072037  
R:Hannum, C.; Culpepper, J.; Campbell, D.; McLanahan, T.; Zurawski, S.; Bazan, J.F.;  
felt, A.; Muench, M.; Kellner, G.; Namiakawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik  
Nature 369, 643-648, 1994  
A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoi  
A:Reference number: S43290; MUID:94195428; PMID:8145851  
A:Accession: S43292  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-71, 'A', '73-235 <HAN>  
A:Cross-references: GB:U04806; NID:g483844; PIDN:AAA17999.1; PID:g483845  
A:Note: the authors translated the codon AGT for residue 25 as Met  
C:Genetics:  
A:Introns: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3

Query Match	Score 1242;	DB 2;	Length 235;
Best Local Similarity	100.0%;	Pred. No. 5.4e-99;	
Matches 235;	Conservative	0; Mismatches	0; Indels
			Gaps 0;
OY	1	MTVLAPAWSPTTYLLLLLLLSGLSGTQCSFQHSPISSDFAVKIRELSDYLLQDYPVY	60
DB	1	MTVLAPAWSPTTYLLLLLLLSGLSGTQCSFQHSPISSDFAVKIRELSDYLLQDYPVY	60
OY	61	ASNLQDEELCGIWRVLVAQRWMERLKTIVAGSKMGLERVTETHEFTKCAFQPPPSCL	120
DB	61	ASNLQDEELCGIWRVLVAQRWMERLKTIVAGSKMGLERVTETHEFTKCAFQPPPSCL	120
OY	121	RFQGTNISRILQETSQVLAQKRWTRQNFRCLELQCPDSSSTLPMPSPPLRATAPV	180
DB	121	RFQGTNISRILQETSQVLAQKRWTRQNFRCLELQCPDSSSTLPMPSPPLRATAPV	180

```

Db      121 RFVQTNISRLLOETSEQLVALKPWITRONFSRCLLELOCOPDSSSTLLPPWMSRPLEATAPL 180
QY      181 APOPELLLLLLLPVGLLLAAAMCLHMQRTRTPRGEQVPPVPSODLLVEH 235
      181 APOPELLLLLLLPVGLLLAAAMCLHMQRTRRKRPRRGEQVPPVPSODLLVEH 235

RESULT 2
S43293
FLT3/FLK2 ligand (clone S109) - human
C:Species: Homo sapiens (man)
C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S43293
R:Hanum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kefel, A.; Muench, M.; Kelnner, G.; Nankawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A.
A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic
A:Reference number: S43290; MUID:94195428; PMID:8145851
A:Accession: S43293
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-245 <HAN>
A:Note: the authors translated the codon AGG for residue 25 as Met

Query Match
Best Local Similarity 69.68; Score 864.5; DB 2; Length 245;
Matches 176; Conservative 7; Mismatches 27; Indels 31; Gaps 3:

QY      1 MTVALPAMSPPTTYLLLLSSGLSGTODCSFQHSPPSSDFAVKIRELSYLLQDYPTV 60
Db      1 MTVALPAMSPPTTYLLLLSSGLSGTODCSFQHSPPSSDFAVKIRELSYLLQDYPTV 60
QY      61 ASNLQDEELCGGLMRLVLAQRMMERLKTVAAGSKMGLLEVRNTEIHFTVKCAFQPPSCL 120
Db      61 ASNLQDEELCGALMRLVLAQRMMERLKTVAAGSKMGLLEVRNTEIHFTVKCAFQPPSCL 120
QY      121 RFVQTNISRLLOETSEQLVALKPWITRONFSRCLLELOCOPG---PRPSGPAACGALT 177
Db      121 RFVQTNISRLLOETSEQLVALKPWITRONFSRCLLELOCOPG---PRPSGPAACGALT 177
QY      181 APOPELLLLLLLPVGLLLAAAMCLHMQRTRTPRGEQVPPVPS 227
Db      178 WPRPHRQEDTEAHRGESP-----ARCGIAMTQKRLAAGSLPAPLIPSP 222
QY      228 Q 228
Db      223 E 223

RESULT 3
I39076
FLT3 ligand alternatively spliced isoform - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: I39076
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.
Oncogene 11, 1165-1172, 1995
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number: I39075; MUID:96032581; PMID:7566977
A:Accession: I39076
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-178 <RES>
A:Cross-references: EMBL:U29874; NID:g1072036; PIDN:AAA90950.1; PID:g1072038
C:Genetics:
A:introns: 11/3; 48/3; 66/3; 114/3; 161/1

Query Match
Best Local Similarity 67.18; Score 834; DB 2; Length 178;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTVALPAMSPPTTYLLLLSSGLSGTODCSFQHSPPSSDFAVKIRELSYLLQDYPTV 60
      1 MTVALPAMSPPTTYLLLLSSGLSGTODCSFQHSPPSSDFAVKIRELSYLLQDYPTV 60

```

```

Db      1 MTVALPAMSPPTTYLLLLSSGLSGTODCSFQHSPPSSDFAVKIRELSYLLQDYPTV 60
QY      61 ASNLQDEELCGGLMRLVLAQRMMERLKTVAAGSKMGLLEVRNTEIHFTVKCAFQPPSCL 120
Db      61 ASNLQDEELCGGLMRLVLAQRMMERLKTVAAGSKMGLLEVRNTEIHFTVKCAFQPPSCL 120
QY      121 RFVQTNISRLLOETSEQLVALKPWITRONFSRCLLELOCOP 160
Db      121 RFVQTNISRLLOETSEQLVALKPWITRONFSRCLLELOCOP 160

RESULT 4
A49265
flt3/FLK-2 ligand precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C:Accession: A49265; I49347; I49346; S43290
R:Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, B.; Holl
D.; Williams, D.E.; Beckmann, M.P.
A:Title: Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase receptor: a
A:Reference number: A49265; MUID:94084791; PMID:7505204
A:Accession: A49265
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-231 <LYM>
A:Cross-references: GB:I23636; NID:g439441; PIDN:AAA93436.1; PID:g439442
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.
Oncogene 11, 1165-1172, 1995
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number: I39075; MUID:96032581; PMID:7566977
A:Accession: I49347
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-163, 'G', 165, 'HYAG' <RES>
A:Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90952.1; PID:g1072041
A:Accession: I49346
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-197, 'L', 198-231 <RES>
A:Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040
R:Hanum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kefel, A.; Muench, M.; Kelnner, G.; Nankawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik
Nature 368, 643-648, 1994
A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic
A:Reference number: S43290; MUID:94195428; PMID:8145851
A:Accession: S43290
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-197, 'L', 198-231 <HAN>
A:Experimental source: clone T110
A:Note: the sequence from Fig. 2c is inconsistent with that from Fig. 2a in having 4-
C:Keywords: transmembrane protein

Query Match
Best Local Similarity 70.38; Score 768.5; DB 2; Length 231;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY      1 MTVALPAMSPPTTYLLLLSSGLSGTODCSFQHSPPSSDFAVKIRELSYLLQDYPTV 59
Db      1 MTVALPAMSPNSLLLLSSGLSGTODCSFQHSPPSSDFAVKIRELSYLLQDYPTV 60
QY      60 VASNLQDEELCGGLMRLVLAQRMMERLKTVAAGSKMGLLEVRNTEIHFTVKCAFQPPSCL 119
Db      61 VAVNLQDEELCGGLMRLVLAQRMMERLKTVAAGSKMGLLEVRNTEIHFTVKCAFQPPSCL 120
QY      120 LRFVQTNISRLLOETSEQLVALKPWITR--QNSRCLLELOCOPDSSSTLLPPWMSRPLEAT 177
Db      121 LRFVQTNISRLLOETSEQLVALKPWITR--QNSRCLLELOCOPDSSSTLLPPWMSRPLEAT 180
QY      178 APTAPQPP--LLLLLPVGLLLAAAMCLHMQRTRRPRRGEQVPPVPS 227

```

Db 181 EUPPEPRROLLLLLLPLTLVLAAMGLRWQRAARR---GELHPGVLP 228

## RESULT 5

SA3291

FLT3/FLK2 ligand (clone 1118) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 17-Mar-1999

C:Accession: SA3291

R:Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; K&amp;

felt, A.; Muench, M.; Kellner, G.; Namiwawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A

Nature 368, 643-648, 1994

A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic

A:Reference number: SA3290; MUID:94195428; PMID:8145851

A:Accession: SA3291

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-220 &lt;HMM&gt;

Query Match 48.8%; Score 606.5; DB 2; Length 220;  
Best local similarity 61.5%; Pred. No. 1.3e-44;  
Matches 134; Conservative 18; Mismatches 43; Indels 23; Gaps 5;

1 MVLAPAWSP-TTYLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSYLLQDPVT 59

1 MVLAPAWSPNSLLLLLSPLCRGTPDCYFHSPISSNFKVRELTDLHLKDYPT 60

60 VASNLQDEELCGGLMRLVLAORMERLKVAGSKMGLERNTETHTKCAFPQPPSC 119

61 VAVNLQDEELCGGLMRLVLAORMERLKVAGSKMGLERNTETHTKCAFPQPPSC 120

120 LRFVQTNISRLQETSEOLVALKPWTR--QNFSCLELQCPDSSSTLPPWSPRP--- 173

121 LRFVQTNISRLKDTQTLALKPCIGKACQNFSCLELQCPDSSSTLPPWSPRP--- 174

174 ---LEATAPTAPOPPLLL-----LLLPVGLLLIAA 201

175 ATRLTATALLTVCPLLPVGTSHMFPLPYFLSLSS 212

## RESULT 6

I58343

flt3 ligand isoform 5H - mouse

C:Species: Mus sp. (mouse)

C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Nov-1999

C:Accession: I58343

R:Lyman, S.D.; James, L.; Escobar, S.; Downey, H.; de Vries, P.; Brasel, K.; Stocking, K

Oncogene 10, 149-157, 1995

A:Title: Identification of soluble and membrane-bound isoforms of the murine flt3 ligand

A:Reference number: I58343; MUID:95124710; PMID:7824267

A:Accession: I58343

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-220 &lt;RES&gt;

A:Cross-references: GB:S76459; NID:9913479; PIDN:AAB33069.1; PID:9913480

Query Match 48.8%; Score 606.5; DB 2; Length 220;  
Best local similarity 61.5%; Pred. No. 1.3e-44;  
Matches 134; Conservative 18; Mismatches 43; Indels 23; Gaps 5;

1 MVLAPAWSP-TTYLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSYLLQDPVT 59

1 MVLAPAWSPNSLLLLLSPLCRGTPDCYFHSPISSNFKVRELTDLHLKDYPT 60

60 VASNLQDEELCGGLMRLVLAORMERLKVAGSKMGLERNTETHTKCAFPQPPSC 119

61 VAVNLQDEELCGGLMRLVLAORMERLKVAGSKMGLERNTETHTKCAFPQPPSC 120

120 LRFVQTNISRLQETSEOLVALKPWTR--QNFSCLELQCPDSSSTLPPWSPRP--- 173

121 LRFVQTNISRLKDTQTLALKPCIGKACQNFSCLELQCPDSSSTLPPWSPRP--- 174

Qy 174 ---LEATAPTAPOPPLLL-----LLLPVGLLLIAA 201

Db 175 ATRLTATALLTVCPLLPVGTSHMFPLPYFLSLSS 212

## RESULT 7

T22672

hypothetical protein F54F12.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T22672

R:Barlow, K.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19597

A:Accession: T22672

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1217 &lt;MIL&gt;

A:Cross-references: EMBL:Z01548; NID:e1062020; PIDN:CAB04464.1; GSPDB:GN00021; CESP:F

A:Experimental source: Clone F54F12

C:Genetics:

A:Gene: CESP:F54F12.1

A:Map position: 3

Query Match 7.5%; Score 93; DB 2; Length 1217;  
Best local similarity 23.6%; Pred. No. 8;  
Matches 38; Conservative 33; Mismatches 68; Indels 22; Gaps 6;

83 MERLKVAGSKMGL---LEAVNTETHTKCAFPQPPSCLEFVQTNISRLQETSEOLV 139

84 MERLKVAGSKMGL---LEAVNTETHTKCAFPQPPSCLEFVQTNISRLQETSEOLV 140

627 MDAVAVDGTGVSSVIDALEKLTMDLDFQYKFKAPATLKAMD---FFASVASNLA 682

140 ALKPWTRQNFSCLELQCPDSSSTL---PPWSPRPLEATAPTAPOPPLLL 191

603 ALRQPTTSDPTAAPVPIPNKKSILNGBSPSPPLPVPVASTPATPATESMMLYII 742

192 LRVGLLLIAA-----AMCLMQRTTRRTPRGEQVPPVPS 227

743 GAVGGLVVALIIGVILFVFFQKKKKEDKPPD--PPAPLP 781

## RESULT 8

TMBE12

74K alpha trans-inducing protein - human herpesvirus 3

C:Species: human herpesvirus 3, varicella-zoster virus

C:Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 16-Jul-1999

C:Accession: C27342

R:Davidson, A.D.; Scott, J.E.

J. Gen. Virol. 67, 1759-1816, 1986

A:Title: The complete DNA sequence of varicella-zoster virus.

A:Reference number: A27345; MUID:86306657; PMID:3018124

A:Accession: C27342

A:Molecule type: DNA

A:Residues: 1-661 &lt;DAV&gt;

A:Cross-references: EMBL:X04370; NID:959989; PIDN:CA27895.1; PID:960001

C:Genetics:

C:Superfamily: herpesvirus 77K alpha trans-inducing protein

C:Keywords: trans-inducing protein; transcription regulation

Query Match 7.4%; Score 92; DB 1; Length 661;  
Best local similarity 26.6%; Pred. No. 4.9;  
Matches 61; Conservative 29; Mismatches 103; Indels 36; Gaps 11;

19 LLSLSLSTQDCS---FQHSPISSDPAVKI--RELSDYLLQDPVTVASNLQDEELCG- 71

79 LTPVLOSTERHVSLLGLHNNVPESLIVSCMSNDVHDGFMQRYMETIQRCIDLDLKGSD 138

72 GLMRLVLAORMERLKVAGSKMGLERVN---TEIHFTKCAFPQPPSCLEFV 123

139 GLM-WVYENTYWOYLKTYTGALEVYSEKVKKSKSYLVLFSSVVAANKPISRHPFKSKI 197









GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 24, 2002, 10:03:41 ; Search time 8.57296 Seconds  
(without alignments)  
1136.939 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242  
Sequence: 1 MTVLAPAWSPTYYLLDLLL.....RPGQVPPVSPQDLLVEH 235

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	1 FLJ3_HUMAN	P49771 homo sapien
2	766	61.8	232	1 FLJ3_MOUSE	P49772 mus musculu
3	92	7.4	661	1 AT12_VZVD	P09264 varicella-2
4	89.5	7.2	941	1 GBR2_HUMAN	075899 homo sapien
5	89	7.2	387	1 SGCA_MESAU	064255 mesocricetu
6	89	7.2	793	1 S3A1_HUMAN	014549 homo sapien
7	87.5	7.0	415	1 TNR3_MOUSE	P50284 mus musculu
8	87.5	7.0	479	1 MPIP_DROME	P20483 drosophila
9	87	7.0	910	1 DDRI_RAT	063474 rattus norv
10	87	7.0	911	1 DDRI_MOUSE	063474 rattus norv
11	86.5	7.0	1394	1 CNG4_BOVIN	028181 bos taurus
12	86	6.9	485	1 SSGP_VOLCA	P21997 volvox cart
13	85	6.8	282	1 ATFS_HUMAN	091241 homo sapien
14	85	6.8	366	1 FCCG_RAT	P13593 rattus norv
15	84.5	6.8	3726	1 ABF1_MOUSE	061323 mus musculu
16	84	6.8	582	1 MNT_HUMAN	099589 homo sapien
17	84	6.8	734	1 YF48_HUMAN	09hcm4 homo sapien
18	84	6.8	1234	1 NPHN_RAT	09hcm4 rattus norv
19	83.5	6.7	671	1 Z282_HUMAN	09udv7 homo sapien
20	83	6.7	758	1 VKGC_HUMAN	P38435 homo sapien
21	82	6.6	2167	1 SHK1_RAT	09v488 rattus norv
22	81.5	6.6	488	1 MMT1_HUMAN	P24347 homo sapien
23	81.5	6.6	591	1 MNT_MOUSE	008789 mus musculu
24	81.5	6.6	2124	1 Y192_HUMAN	093074 homo sapien
25	81	6.5	283	1 ATFS_MOUSE	070101 mus musculu
26	81	6.5	387	1 SGCA_MOUSE	P82350 mus musculu
27	81	6.5	428	1 EPC_HUMAN	P01854 homo sapien
28	81	6.5	1248	1 DIAL_HUMAN	060610 homo sapien
29	80.5	6.5	1402	1 IF4G_RABIT	P41110 oryctolagus
30	80	6.4	397	1 CEF3_STRCL	P18549 streptomyces
31	80	6.4	940	1 GBR2_RAT	088871 rattus norv
32	80	6.4	1174	1 KPC1_COCHF	042632 cochlidochl
33	80	6.4	1794	1 YAV1_SCHPO	010172 schizosacch

## ALIGNMENTS

RESULT 1	FLJ3L_HUMAN	STANDARD;	PRT;	235 AA.
AC	P49771;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (Flt3 ligand) (Flt3l).			
GN	FLT3LG.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94195428; PubMed=8145851;			
RA	Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S., Bazen J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J., Muench A., Keiner G., Namioka R., Kennick D., Roncarolo M.G., Zlotnick A., Rosnet O., Dubreuil P., Birbaum D., Lee F.;			
RA	"Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic stem cells and is encoded by variant RNAs."			
RT	Nature 368:643-648(1994).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94235842; PubMed=8180375;			
RA	Lymon S.D., James L., Johnson L., Brasel K., de Vries P., Escobar S.S., Downey H., Splett R.R., Beckmann M.P., McKenna H.J.;			
RT	"Cloning of the human homologue of the murine flt3 ligand: a growth factor for early hematopoietic progenitor cells."			
RL	Blood 83:2795-2801(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.			
RX	MEDLINE=96032581; PubMed=7566977;			
RA	Lymon S.D., Stocking K., Davison B., Fletcher F., Johnson L., Escobar S.;			
RT	"Structural analysis of human and murine flt3 ligand genomic loci."			
RL	Oncogene 11:1165-1172(1995).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).			
RX	MEDLINE=20343011; PubMed=10881197;			
RA	Savvides S.N., Boone T., Karplus P.A.;			
RT	"Flt3 ligand structure and unexpected commonalities of helical bundles and cysteine knots."			
RL	Nat. Struct. Biol. 7:486-491(2000).			
CC	- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING FACTORS AND INTERLEUKINS.			
CC	- SUBUNIT: Homodimer (isoform 2).			
CC	- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1); secreted (isoform 2).			
CC	- ALTERNATIVE PRODUCTS: 2 isoforms; a 1/membrane-bound (shown here) and 2/soluble; are produced by alternative splicing.			
CC				

RESULT 2			
FL3L_MOUSE			
ID	FL3L_MOUSE	STANDARD:	PRT: 232 AA.
AC	P49772; Q64085;		
DDT	01-OCT-1996 (Rel. 34, Created)		
DDT	01-OCT-1996 (Rel. 34, Last sequence update)		
DDT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	SL cytokine precursor (fms-related tyrosine kinase 3 ligand) (FL3L ligand) (FL3L).		
DE	FL3LG OR FL3L.		
GN	Fms musculus (Mouse).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NCBI_TaxID=10090;			
[1]			
RRN	SEQUENCE FROM N.A.		
RRP	MEDLINE=94195428; PubMed=8145851;		
XX			

RA Hannum, Culpepper J., Campbell D., McClanahan T., Zurawski S.,  
RA Bazar J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J.,  
RA Duda G., Martina N., Peterson D., Menon S., Shinafelt A.,  
RA Wuensch A., Keiner G., Namikawa R., Rennick D., Roncarolo M.G.,  
RA Joltnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.,  
RT "Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of  
RT hematopoietic stem cells and is encoded by variant RNAs.",  
RN Nature 368:643-648(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-STL/J;  
RX MEDLINE=94084791; PubMed=7505204;  
RA Lyman S.D., James L., Vandenbos T., Devries P., Brasel K.,  
RA Gliniak B., Hollingsworth L.T., Picha K.S., McKenna H.J.,  
RA Spielt R.R., Fletcher F.A., Maraskovsky E., Farrar T.,  
RA Foxworth D., Williams D.E., Beckmann M.P.;  
RT "Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase  
RT receptor: a proliferative factor for primitive hematopoietic cells";  
RL Cell 75:1157-1167(1993).  
RN [3]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=96032581; PubMed=7569977;  
RA Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,  
RA Escobar S.;  
RT "Structural analysis of human and murine flt3 ligand genomic loci";  
RN Oncogene 11:1165-1172(1995).  
RN [4]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=95124710; PubMed=7824267;  
RA Lyman S.D., James L., Escobar S., Downey H., de Vries P.,  
RA Brasel K., Stocking K., Beckmann M.P., Copeland N.G.,  
RA Cleveland L.S.;  
RT "Identification of soluble and membrane-bound isoforms of the murine  
RT flt3 ligand generated by alternative splicing of mRNAs";  
RN Oncogene 10:149-157(1995).  
RN [5]  
RP SEQUENCE FROM N.A.  
RA McClanahan T., Culpepper J., Campbell D., Wagner J.,  
RA Franz-Bacon K., Mattson J., Tsai S., Luh J., Guimares M.J.,  
RA Mattei M.-G., Rosnet O., Birnbaum D., Hannum C.;  
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
CC -! FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC  
CC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING  
CC FACTORS AND INTERLEUKINS.  
CC -! SUBUNIT: Homodimer (soluble isoform) (By similarity).  
CC -! SUBCELLULAR LOCATION: Type I membrane protein. Two soluble  
CC isoforms are also produced by alternative splicing. One of which,  
CC isoform 3/E6, is biologically active, while the other, isoform  
CC 4/E6delta1a6, is inactive.  
CC -! ALTERNATIVE PRODUCTS: 4 isoforms: 1/6C (shown here), 2/5H, 3/E6  
CC and 4/E6delta1a6; are produced by alternative splicing.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC at the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: U04807; AAA18000.1; -  
DR EMBL: L23636; AAA33436.1; -  
DR EMBL: U29875; AAA90951.1; -  
DR EMBL: U29875; AAA90952.1; -  
DR EMBL: S76459; AAB33068.1; -  
DR EMBL: S76461; AAB33070.1; -  
DR EMBL: S76464; AAB33071.1; -  
DR EMBL: U44024; AAA93307.1; -  
DR EMBL: U44024; AAA93306.1; -  
DR MGD: MGI:95560; Flt3l.  
DR InterPro: IPR004213; Flt3l\_1lg.  
DR Pfam: PF02947; flt3\_1lg; 1.  
RW cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal.

```

FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 232 SL CYTOKINE.
FT DOMAIN 27 189 EXTRACELLULAR (POTENTIAL).
FT TRAMSMEM 190 210 POTENTIAL.
FT DOMAIN 211 232 CYTOPLASMIC (POTENTIAL).
FT DISULFID 31 112 BY SIMILARITY.
FT DISULFID 71 156 BY SIMILARITY.
FT DISULFID 120 161 BY SIMILARITY.
FT CAROHD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPIC 164 232 DSSLPRSPALAELELPPEPRRLILLILLPLTVL
LAAMGLMORARRGELPVPPLPSHH -> GNGGPAOH
HGATRLTALITVCPGLLPPLVGTSHHFLPYLSLSST
FT FT LKMTYV (IN ISOFORM 2).
FT VARSPIC 164 169 DSSL -> GSHYAG (IN ISOFORM 3).
FT VARSPIC 170 232 MISSING (IN ISOFORM 3).
FT VARSPIC 159 163 VOCOP -> GLIMORALTLNKSOSCLVLSAGIT (IN
ISOFORM 4).
FT CONFLICT 141 141 A -> G (IN REF. 1).
FT CONFLICT 198 198 MISSING (IN REF. 2).
SQ SEQUENCE 232 AA; 26141 MW; 3A3680D3CB69FBAB CRC64;

```

```

Query Match 61.8%; Score 768; DB 1; Length 232;
Best Local Similarity 70.0%; Pred. No. 3.6e-57;
Matches 163; Conservative 17; Mismatches 43; Indels 10; Gaps 4;

```

```

QY 1 MVLAPAMSP-TTTLILLILLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLDQDEVT 59
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 MVLAPAMSPNSLLILLILLSPCLRGTPDCYFSSHSNKVRFELTHLLKDYPT 60
VASNLODELGCGLMRVLAORMERIKTVASGKMOGLLENTLHVTKAPRPPSC 119
61 VAVNIODEHNCALMSLFLAQRMTEOLKTVAASKMOTLEEDVNTLHVTSCTFQPLEEC 120
QY 120 LRFVQNTNIRLQETSEQLVALKPMITR--QNSRCLQLQCPDSTLPPWSPRLBAT 177
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 121 LRFVQNTNIRLQETSEQLVALKPMITR--QNSRCLQLQCPDSTLPPWSPRLBAT 177
121 LRFVQNTNIRLQETSEQLVALKPMITR--QNSRCLQLQCPDSTLPPWSPRLBAT 180
QY 178 APTAPQP--LLILLPLVGLLLLAAMWCLHMORTRRTPRPGSQVPPVSP 227
1:1 ||||| : : : : : : : : : : : : : : : : : : : : :
DB 181 ELPEPRRLILLILLILLPLTVLTLAAAGLMMORARR--GELHPCVPLP 229

```

```

RESULT 3
AT12_VZVD STANDARD: PRT; 661 AA.
AC P09264;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Alpha trans-inducing factor 74 kDa protein.
GN 12.
OS Varicella-zoster virus (strain Dumas) (VZV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_TaxID=10338;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8630657; PubMed=3018124;
RA Davison A.J., Scott J.E.;
RT "The complete DNA sequence of varicella-zoster virus.";
RL J. Gen. Virol. 67:1759-1816(1986).
CC -1- FUNCTION: MODULATE ALPHA TRANS-INDUCING FACTOR-DEPENDENT
ACTIVATION OF ALPHA GENES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib.ch)
CC -----

```

```

DR EMBL: X04370; CAA27895.1; -.
DR PIR: C27342; TNBE12.
DR InterPro: IPR005051; Herpes_UL46.
DR Pfam: PF03387; Herpes_UL46; 1.
KW Transcription regulation; Trans-acting factor.
SQ SEQUENCE 661 AA; 74272 MW; C5CA77A160365379 CRC64;

```

```

Query Match 7.4%; Score 92; DB 1; Length 661;
Best Local Similarity 26.6%; Pred. No. 2.7;
Matches 61; Conservative 29; Mismatches 103; Indels 36; Gaps 11;

```

```

QY 19 LLSGLSGTQDCS----FOHSPISSDFAVKI--RELSDYLLQDEVTVAASNLODEELCG- 71
| | | | | : : : : : : : : : : : : : : : : : : : : :
DB 79 LTFVYLQSTERNHSHVLLGLHNNNPESLVSCKNSNDVHDGMQKXMETIQRCLEDDLKSGD 138
QY 72 GLMLVLAORMERIKTVASGKMOGLLERYN----TEIHFTKAFQP--PPSCLREV 123
| | | : : : : : : : : : : : : : : : : : : : : :
DB 139 GLW-WVENYTWQVLKVTGAEVPTSEKVNKKSSTVLLFSSVAVANKPISRHPFKSVI 197
QY 124 QTNISRLQETSEQLVALKPMITRONSRCLQLQCPDSTLPPWSP-RPLEATAPAP 182
: : : : : : : : : : : : : : : : : : : : :
DB 198 NSDVRGICQELREALGAVQKM--YFMR-----PDDPTNPSPTIRIKVQETIAAYTAP 247
QY 183 QPRLILLILLPVGLLLLAAMWCLHMORTRRTPRPGSQVPPVSPDPL 231
: | | | | : : : : : : : : : : : : : : :
DB 248 GYGMMLNPLVDVYD-----ARVCRHLKLFRRIRNGFRASY-----IPDDL 287

```

```

RESULT 4
GBR2_HUMAN STANDARD: PRT; 941 AA.
ID GBR2_HUMAN
AC 075899; 075974; 075975; Q9UN99; Q9UNR1; Q9P1R2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gamma-aminobutylic acid type B receptor, subunit 2 precursor (GABA-B
DE 51) (GPR 51) (HG20).
GN GABBR2 OR GPR51.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RC TISSUE=Cerebellum;
RX MEDLINE=99087321; PubMed=9872316;
RA White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H.,
RA Barnes A.A., Emson P., Foord S.M., Marshall F.H.;
RT "Heterodimerization is required for the formation of a functional
RT GABA(B) receptor.";
RL Nature 396:679-682(1998).
RN [2]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 2A; 2B AND 2C).
RC TISSUE=Brain;
RX MEDLINE=20193514; PubMed=10727622;
RA Clark J.A., Mezey E., Lam A.S., Bonner T.T.;
RT "Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";
RL Brain Res. 860:41-52(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RA Lin M., Parker R., Mccrea K., Watson J., Baker E., Sutherland G.,
RA Herzog H.;
RT "Cloning and characterization of a novel human GABA-B receptor subtype
RT with high affinity for GABA and low affinity for baclofen.";
RL submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RC TISSUE=Hippocampus;
RA Botowoky B., Laz T., Gerald C.;
RL submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2A).

```

CC TISSUE-Fetal brain;  
 RX MEDLINE=99189236; PubMed=10087195;  
 RA Ng G.Y.K., McDonald T., Bonnett T., Rigby M., Heavens R., Whiting P.,  
 RA Chateauf A., Coulombe N., Kargman S., Caskey T., Evans J.F.,  
 RA O'Neill G.P., Liu Q.,  
 RT "Cloning of a novel G-protein-coupled receptor GPR 51 resembling GABAB  
 RT receptors expressed predominantly in nervous tissues and mapped  
 RT proximal to the hereditary sensory neuropathy type 1 locus on  
 RT chromosome 9.";  
 RL Genomics 56:288-295(1999).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 2A), AND VARIANTS PHE-628 AND ALA-869.  
 RC TISSUE-Brain;  
 RX MEDLINE=99263199; PubMed=10328880;  
 RA Martin S.C., Russek S.J., Farb D.H.;  
 RT "Molecular identification of the human GABABR2: cell surface  
 RT expression and coupling to adenylyl cyclase in the absence of  
 RT GABABR1.";  
 RL Mol. Cell. Neurosci. 13:180-191(1999).  
 RN [7]  
 RP R1A-R2 INTERACTION.  
 RX MEDLINE=99175124; PubMed=10075644;  
 RA Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan R.,  
 RA Kargman S., Chateauf A., Tsukamoto N., McDonald T., Whiting P.,  
 RA Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,  
 RA Bonner T.I., O'Neill G.P.;  
 RT "Identification of a GABAB receptor subunit, gb2, required for  
 RT functional GABAB receptor activity.";  
 RL J. Biol. Chem. 274:7607-7610(1999).  
 RN [8]  
 RP R1A-R2 INTERACTION.  
 RX MEDLINE=20237752; PubMed=10773016;  
 RA Sullivan R., Chateauf A., Coulombe N., Kolakowski L.F. Jr.,  
 RA Johnson M.P., Hebert T.E., Ethier N., Belley M., Metters K.,  
 RA Abramovitz M., O'Neill G.P., Ng G.Y.K.;  
 RT "Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B))  
 RT receptors with truncated receptors and metabotropic glutamate  
 RT receptor 4 supports the GABA(B) heterodimer as the functional  
 RT receptor.";  
 RL J. Pharmacol. Exp. Ther. 293:460-467(2000).  
 CC -1- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS  
 CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,  
 CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,  
 CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES  
 CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE  
 CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC  
 CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING  
 CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC  
 CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT  
 CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE  
 CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN  
 CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM  
 CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND  
 CC ANTINOCICEPTION.  
 CC -1- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH  
 CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO  
 CC HAPPEN.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER  
 CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A  
 CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE  
 CC PLASMA MEMBRANE.  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: 2A (SHOWN HERE), 2B AND 2C; ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN  
 CC CEREBRAL CORTEX, THALAMUS, HIPPOCAMPUS, FRONTAL, OCCIPITAL AND  
 CC TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLUM, FOLLOWED BY CORPUS  
 CC CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, AMYGDALA AND MEDULLA.  
 CC WEALY EXPRESSED IN HEART, TESTIS AND SKELETAL MUSCLE.  
 CC -1- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION  
 CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
 CC GABA-B RECEPTOR SUBFAMILY.  
 CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>  
 CC or send an email to [license@isb.ch](mailto:license@isb.ch)).  
 CC -----  
 DR EMBL; AJ012188; CAA09942.1; -  
 DR EMBL; AF056085; AAC63228.1; -  
 DR EMBL; AF095723; AAC63383.1; -  
 DR EMBL; AF095724; AAC63384.1; -  
 DR EMBL; AF095784; AAD30389.1; -  
 DR EMBL; AF074483; AAD03336.1; -  
 DR EMBL; AF069755; AAC99345.1; -  
 DR EMBL; AF099033; AAD45867.1; -  
 DR Genew; HGNC:4507; GPR51.  
 DR InterPro; IPR001828; ANF\_receptor.  
 DR InterPro; IPR000337; GPCR\_Mgr.  
 DR Pfam; PF01094; ANF\_receptor; 1.  
 DR Pfam; PF00003; 7tm\_3; 1.  
 DR PROSITE; PS00979; G-PROTEIN\_RECPE\_F3\_1; FALSE\_NEG.  
 DR PROSITE; PS00980; G-PROTEIN\_RECPE\_F3\_2; FALSE\_NEG.  
 DR PROSITE; PS00981; G-PROTEIN\_RECPE\_F3\_3; FALSE\_NEG.  
 DR PROSITE; PS0259; G-PROTEIN\_RECPE\_F3\_4; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 KW Postsynaptic membrane; Coiled coil; Alternative splicing;  
 KW Polymorphism.  
 KM SIGNAL 1 41  
 FT CHAIN 42 941  
 FT  
 FT DOMAIN 42 483  
 FT TRANSMEM 484 504  
 FT DOMAIN 505 522  
 FT TRANSMEM 523 543  
 FT DOMAIN 544 551  
 FT TRANSMEM 552 572  
 FT DOMAIN 573 597  
 FT TRANSMEM 598 618  
 FT DOMAIN 619 654  
 FT TRANSMEM 655 675  
 FT DOMAIN 676 691  
 FT TRANSMEM 692 712  
 FT DOMAIN 713 720  
 FT TRANSMEM 721 741  
 FT DOMAIN 742 941  
 FT DOMAIN 781 819  
 FT CARBOHYD 90 90  
 FT CARBOHYD 298 298  
 FT CARBOHYD 389 389  
 FT CARBOHYD 404 404  
 FT CARBOHYD 453 453  
 FT CARBOHYD 902 927  
 FT VARSPLIC 929 941  
 FT  
 FT VARIANT 628 628  
 FT  
 FT VARIANT 869 869  
 FT  
 FT CONFLICT 6 6  
 FT CONFLICT 12 12  
 FT CONFLICT 424 424  
 FT  
 FT SEQUENCE 941 AA; 105821 MW; 09F1773DB0673C5D CRC64;  
 SO  
 Query Match 7.28; Score 89.5; DB 1; Length 941;  
 Best Local Similarity 44.13;  
 Matches 26; Conservative 2; Mismatches 22; Indels 9; Gaps 3;  
 Oy 170 SPRPLENTAPAPDP-----LILLILLPVGLLLAAMCWMQRTRRTRRPEGEQPVV 224  
 Db 3 SPKSGGPGPPPPPPPPPARLLLLPLLLPLAPGAW--GW--ARGAPRPPSPPL 56

ID	SCGA_MESAU	STANDARD;	PRT;	387 AA.
SCGA_MESAU				
AC	Q64235;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Alpha-sarcoglycan precursor (Alpha-SG) (adhalin) (50 kDa dystrophin-associated glycoprotein) (50DAG).			
DE	SCGA.			
GN				
OS	Mesocricetus auratus (Golden hamster).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;			
OC	Mesocricetus			
OX	NCBI_TaxID=10036;			
OX	[1]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=Syrian; TISSUE=Heart muscle;			
RC	MEDLINE=98054328; PubMed=93911120;			
RX				
RA	Sakamoto A., Ono K., Abe M., Jasmijn G., Eki T., Murakami Y.,			
RA	Maekai T., Toyooka T., Hanaka F.;			
RT	"Both hypertrophic and dilated cardiomyopathies are caused by mutation			
RT	of the same gene, delta-sarcoglycan, in hamster: an animal model of			
RT	disrupted dystrophin-associated glycoprotein complex.";			
TL	Proc. Natl. Acad. Sci. U.S.A. 94:13875-13878(1997).			
121				

RP SEQUENCE FROM N.A.  
RC STRAIN=FB: TISSUE=Skeletal muscle;  
RX MEDLINE=95278335; PubMed=7758576;  
RA Roberts S.L., Campbell K.P.;  
RT "Adhalin mRNA and cDNA sequence are normal in the cardiomyopathic  
RT hamster.";  
RL FEBS Lett. 364:245-249(1995).  
CC -I- FUNCTION: COMPONENT OF THE SARCOGLYCAN COMPLEX, A SUBCOMPLEX OF  
CC THE DYSTROPHIN-GLYCOPROTEIN COMPLEX WHICH FORMS A LINK BETWEEN THE  
CC F-ACTIN CYTOSKELETON AND THE EXTRACELLULAR MATRIX.  
CC -I- SUBCELLULAR LOCATION: Type I membrane protein. Sarcoplasmal  
CC (potential).  
CC -I- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN SKELETAL AND  
CC HEART MUSCLE.  
CC -I- SIMILARITY: BELONGS TO THE SARCOGLYCAN ALPHA/EPSILON FAMILY.  
CC -----

CC	THIS SMS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION	
CC	CC BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION -	
CC	CC THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS	
CC	CC USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY	
CC	CC MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL	
CC	CC ENTITIES REQUIRES A LICENSE AGREEMENT (SEE <a href="http://www.isb.ch/announce/isb-sib.ch">HTTP://WWW.ISB.CH/ANNOUNCE/ISB-SIB.CH</a> ).	
CC	CC OR SEND AN EMAIL TO <a href="mailto:license@isb-sib.ch">LICENSE@ISB-SIB.CH</a> ).	
DR	EMBL; D83651; BAA12025.1; -	
DR	EMBL; U21677; AAA81645.1; -	
KW	Cytoskeleton; Transmembrane; Glycoprotein; Signal.	
FT	FT SIGNAL; 1 23	POTENTIAL.
FT	FT CHAIN 24 387	ALPHA-SARCOGLYCAN.
FT	FT DOMAIN 24 290	EXTRACELLULAR (POTENTIAL).
FT	FT TRANSMEM 291 311	POTENTIAL.
FT	FT DOMAIN 312 387	CYTOPLASMIC (POTENTIAL).
FT	FT DOMAIN 209 335	CYS-RICH.
FT	FT CARBOHYD 174 174	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT CARBOHYD 246 246	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT CARBOHYD 387 AA; 43326 MW;	D8599C0FAF646C3F CRC64;
Q	SEQUENCE	

```

Query Match      7.28; Score 89; DB 1; Length 387;
Best Local Similarity 23.48; Pred. NO. 2.6;
Matches 71; Conservative 26; Mismatches 97; Indels 110; Gaps 14;

QY    11 TTYVLLLLSSGLSGTQCDFOHSPISSDPAVRKIRELSDYLDDYPYTVASNLQDEELC 70
      || ||||| :||:::||::||::||::||::||::||::||::||::||::||:
Db     115 TTTRRLTLII-----EDPEGPRLPQAERLVASHDVEVL-----PSTANRFL--IAL 161
      ||||| |         :||::||::||::||::||::||::||::||::||:

QY    71 GGLMRL-----VLAQRMRERLKTYAGSMMOGLLERVNTEIHPVT-----K 110
      ||||| |         :||::||::||::||::||::||::||::||::||:

```

[illegible]

RESULT	6
33A1_HUMAN	
ID	33A1_HUMAN
AC	Q15459;
DT	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Splicing factor 3 subunit 1 (Spliceosome associated protein 114) (SAP114) (SF3a120).
GN	SF3A1 OR SAP114.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=96079958; PubMed=7489498;
RA	Kraemer A., Mulhouser F., Wersig C., Groning K., Bilbe G.;
RT	"Mammalian splicing factor SF3a120 represents a new member of the
RT	SUPR family of proteins and is homologous to the essential splicing
RT	factor PRP19 of <i>Saccharomyces cerevisiae</i> .";
RL	RNA 1:260-272(1995).

RP SEQUENCE FROM N.A.  
RX MEDLINE=200571165; PubMed=10591208;  
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,  
RA Camp M., Smink L.J., Ainscough R., Almeida J.P., Babbae A.K.,  
RA Bagnall C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,  
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,  
RA Burfell W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,  
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,  
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,  
RA Dhami P.D., Dockree C., Dodsworth S.J., Dublin R.M., Ellingham A.G.,  
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,  
RA Gilbert J.G.R., Goward M.E., Graffham D.V., Griffiths M.N.D., Hall C.,  
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S.S., Holmes S.,  
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,  
RA Laird G.K., Langford C.F., Leverstra M.A., Lloyd C., Lloyd D.M.,  
RA Marlyn I.D., Mashreght-Mohammadi M., Matthews L.H., McLean O.T.,  
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,  
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,  
RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L.,  
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,  
RA Soderlund C., Spragun L., Steward C.A., Sulston J.E., Swann R.M.,  
RA Vandin M., Walli M., Wallis J.M., Whiteley M.N., Willey D.L.,  
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,  
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,  
RA Minoshima S., Kawasaki K., Sasaki T., Aakawa S., Kudoh J.,  
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyma S.,  
RA Roe B.A., Chen F., Chu L., Chubb J., Deschamps S., Do A., Do T.,  
RA Dorman A., Fang F., Fu Y., Hu P., Huai A., Kenton S., Lai H.,  
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,  
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,  
RA Wang Q., Wang Y., Wang Z., White D., Willingham D., Wu H., Yao Z.,

RA Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,  
RA Fulcon R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,  
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,  
RA Hinds K., Kemp K., Latreille P., Layman D., Ozerisky P., Rohlfing T.,  
RA Schet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,  
RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,  
RA Emanuel H.E., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,  
RA McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,  
RA Kim U.J., Shizuya H., Simon M.L., Dunamski J.P., Feyard M., Kedra D.,  
RA Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,  
RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,  
RA Tilahun Y., Wright H.;  
RT "The DNA sequence of human chromosome 22.";  
RL Nature 402:489-495(1999).  
RN [3]  
RP CHARACTERIZATION OF THE SPLICEOSOME.  
RX MEDLINE=20337962; PubMed=10882114;  
RA Das R., Zhou Z., Reed R.;  
RT "Functional association of U2 snRNP with the ATP-independent  
RT spliceosomal complex E";  
RL Mol. Cell 5:779-787(2000).  
CC -|- FUNCTION: SUBUNIT OF THE SPLICING FACTOR SF3A REQUIRED FOR 'A'  
CC COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE  
CC BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT  
CC BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS  
CC ESSENTIAL. IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE  
CC INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX.  
CC -|- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3A WHICH IS COMPOSED OF  
CC THREE SUBUNITS: SF3A3/SAP61, SF3A2/SAP62, SF3A1/SAP114. SF3A  
CC ASSOCIATES WITH THE SPLICING FACTOR SF3B AND A 12S RNA UNIT TO  
CC FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX (U2 SNRNP).  
CC INTERACTS WITH SF3A3.  
CC -|- SUBCELLULAR LOCATION: Nuclear (By similarity).  
CC -|- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.  
CC -|- SIMILARITY: CONTAINS 1 UBQUITIN-LIKE DOMAIN.  
CC -|- SIMILARITY: TO YEAST PRE-MRNA SPLICING FACTOR PRP21.  
CC -|-  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: X85237; CAAS9494.1; -  
CC EMBL: AC004997; AAC23435.1; -  
CC DR HSSP: Q15843; INDG.  
CC DR GeneW: HGNC:10765; SF3A1.  
CC DR MIM: 605595; -  
CC DR InterPro: IPR000061; Surp.  
CC DR InterPro: IPR000626; Ubiquitin.  
CC DR Pfam: PF00240; Ubiquitin; 1.  
CC DR Pfam: PF01805; Surp; 2.  
CC DR SMART: SM00213; UBO; 1.  
CC DR PROSITE: PS50053; UBQUITIN\_2; 1.  
CC DR Spliceosome; mRNA processing; mRNA splicing; Nuclear protein; Repeat.  
CC KM REPEAT 52 94 SURP MOTIF 1.  
CC FT REPEAT 166 208 SURP MOTIF 2.  
CC FT DOMAIN 707 793 UBQUITIN-LIKE.  
CC FT DOMAIN 10 16 POLY-PRO.  
CC FT DOMAIN 118 122 POLY-GLN.  
CC FT DOMAIN 260 267 POLY-GLU.  
CC FT DOMAIN 369 372 POLY-PRO.  
CC FT DOMAIN 557 560 POLY-PRO.  
CC FT DOMAIN 672 675 POLY-PRO.  
CC SQ SEQUENCE 793 AA; 88886 MW; 7259FIEC4577305C CRC64;

Query Match 7.2%; Score 89; DB 1; Length 793;  
Matches 67; Conservativity 34; Mismatches 79; Indels 120; Gaps 17;  
4 LAPAWSPTVLLLLLSGLSGTODCSFOHSPISDFAVKIRELSDYLLDYPVTVAAS 63

Db 401 LPPAPADDEVLY-----SPITGE--KI-----PASK 424  
Qy 64 LDEELCGGRLVLAORME-RLKTV-----AGSKMOGLLEVNTEIHF 107  
Db 425 MOEHRIG-----LIDRMEFORDRSIREKQSDDEVYAPGLDISSIKLAEE-RTDIFG 478  
Qy 108 VTKCA-----FOPPSCLR-----VQTNISRLLOETSEQVALKPMI 145  
Db 479 VEEFAIGKKGEEETQKPEEKVTWDGSGSMARQQAQANT--LQEQLEAIHKAGLV 536  
Qy 146 ---TRQNF--SRCLERQCP-----DSSTLP-----PPWSRPLEAT---APT 180  
Db 537 PEDDTKEIGSKRNEIQQDPPPSATINIPSSAPITSVPRPTMPPPVRTTVSAVPP 596  
Qy 181 APQPLLILLIPGILLILAAACLIHQRR-----RTPRGGEVPP---VPSR 227  
Db 597 MPRPPMASVRLPPGVSIVAPMPLIHAPRINVVMPSPADPIMAPRPPMIVETAFVAP 656

## RESULT 7

TNR3\_MOUSE STANDARD; PRT; 415 AA.  
AC P50284;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 3 precursor  
DE (Lymphotoxin-beta receptor).  
GN LTBR OR TNFRSF3 OR TNFR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CVB; TISSUE=Lung;  
RX MEDLINE=96072804; PubMed=7594541;  
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,  
RA Browning J.L., Ware C.F.;  
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,  
RT and expression.";  
RL J. Immunol. 155:5280-5288(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96163885; PubMed=8586432;  
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,  
RA Honjo T.;  
RT "The murine lymphotoxin-beta receptor cDNA: Isolation by the signal  
RT sequence trap and chromosomal mapping.";  
RL Genomics 30:312-315(1995).  
CC -|- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing  
CC LTR and LTB, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3  
CC and TRAF5. May play a role in the development of lymphoid organs  
CC (By similarity).  
CC -|- SUBUNIT: Self-associates (By similarity).  
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -|- SIMILARITY: CONTAINS 4 TNR-CYS REPEATS.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: U29173; AAA68964.1; -  
CC DR EMBL: L38423; AAB00846.1; -  
CC DR EMBL: U30798; AAB81334.1; -  
CC DR HSSP: O14763; IDOG.  
CC DR MGD: MGI:104875; Ltbr.  
CC DR InterPro: IPR001368; TNFR\_c6.



```
DR Pfam: PF00020; TNFR_C6; 3.
DR Pfam: PD000771; TNFR_C6; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00505; TNFR_NGFR_2; 3.
DR Receptor: Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 415
FT DOMAIN 31 223
FT TRANSMEM 224 244
FT REPEAT 245 415
FT REPEAT 42 81
FT REPEAT 125 170
FT REPEAT 171 213
FT REPEAT 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 150
FT DISULFID 142 169
FT DISULFID 172 187
FT CARBOHYD 179 40
FT CARBOHYD 179 40
SQ SEQUENCE 415 AA; 44956 MW; 29B326A56AE661 CRC64;

Query Match
Best local similarity 24.4%; Pred. No. 3; 7;
Matches 39; Conservative 20; Mismatches 52; Indels 49; Gaps 8;

QY 110 KCAFPPEPCL-----REV-----QTNISRLLOETSDQVALKPKWITRONFS 151
DB 123 ECRGQGMSCVYLIDNECVHCEERLVLQCPGTEAEVTDIMTDVNCVCCKGHRQNNSS 182
QY 152 RCELCGCGDSSLTTPPMSPPRLPEATP-----TAPRPPLLLLLLVGLL--- 198
DB 183 P-RARCGPHTRC-----EIQGLVEAPAGTSTSDTICKNPBPGAMLLAILLSLVFL 235
QY 199 ----LAAACLMHQRTR-----RRTPRGEOVPVPVSPQ 228
DB 236 FTTVTLACAMRHPSLCRKLTGLTKRHP-GEESPCCPAPR 274

RESULT 8
MPP_DROME STANDARD; PRT; 479 AA.
AC P20483; O9VAL9;
DT 01-FEB-1991 (rel. 17, Created)
DT 16-OCT-2001 (rel. 40, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE M-phase inducer phosphatase (EC 3.1.3.48) (String protein) (Cdc25-like
DE protein).
DE STG OR CDC25 OR GGI395.
GN Drosophila melanogaster (Fruit fly).
OS Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89195217; PubMed=2702688;
RT Edgar B.A., O'Farrell P.H.;
RL "Genetic control of cell division patterns in the Drosophila embryo.";
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91006056; PubMed=2120044;
RT Jimenez J., Aliphey L., Nurse P., Glover D.M.;
RL "Complementation of fission yeast cdc2ts and cdc25ts mutants
```

```
RT Identifies two cell cycle genes from Drosophila: a cdc2 homologue and
RT string.";
RL EMBO J. 9:3565-3571(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Broksstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Glaser C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,
RA Jaisl M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclby J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -i- FUNCTION: THIS PROTEIN FUNCTIONS AS A DOSAGE-DEPENDENT INDUCER IN
CC MITOTIC CONTROL. IT IS A TYROSINE PROTEIN PHOSPHATASE REQUIRED FOR
CC PROGRESSION OF THE CELL CYCLE. IT MAY DIRECTLY DEPHOSPHORYLATE
CC P34(CDC2) AND ACTIVATE THE P34(CDC2) KINASE ACTIVITY.
CC -i- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -i- SIMILARITY: BELONGS TO THE MPI PHOSPHATASE FAMILY.
CC -i- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch.)
CC
CC EMBL: M24909; AAA28916.1; -
CC EMBL: X57495; CAA40732.1; -
CC EMBL: AE0033768; AAF56885.1; -
CC PIR: A32290; A32290.
CC PIR: S12008; S12008.
CC HSP: P30304; 1C25.
CC FlyBase: FBgn0003525; stg.
CC InterPro: IPR000751; MPI_Phosphatase.
CC InterPro: IPR001763; Rhodanese-like.
CC Pfam: PF00581; Rhodanese; 1.
CC PRINTS: PR00716; MPIPHPHASE.
```



DE (DDR) (Discoïdin receptor tyrosine kinase) (Protein-tyrosine kinase  
MPK-6).  
GN DDR1 OR EDDR1 OR CAK OR MPK6.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RC STRAIN=C57BL/6;  
RX MEDLINE=96204002; PubMed=862263;  
RT Perez J.L., Jing S.O., Wong T.W.;  
RT "Identification of two isoforms of the Cak receptor kinase that are  
RT coexpressed in breast tumor cell lines."  
RL Oncogene 12:1469-1477(1996).  
RN [2]  
RP SEQUENCE OF 766-822 FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Embryonic brain;  
RX MEDLINE=93096484; PubMed=1281307;  
RA Giaraldi-Hebenstreit P., Nieto M.A., Frahn M., Mattei M.-G.,  
RA Chetlier A., Wilkinson D.G., Charney P.;  
RT "An Eph-related receptor protein tyrosine kinase gene segmentally  
RT expressed in the developing mouse hindbrain."  
RL Oncogene 7:2499-2506(1992).  
CC -1- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND  
CC RECOGNITION (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
CC tyrosine phosphate.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CAK I (SHOWN HERE) AND CAK II;  
CC ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER BY THE  
CC ABSENCE OF A 37 RESIDUES SEGMENT.  
CC -1- TISSUE SPECIFICITY: THE PREDOMINANT ISOFORM CAK I, IS EXPRESSED IN  
CC DEVELOPING EMBRYO AND ADULT BRAIN; CAK II IS EXPRESSED IN VARIOUS  
CC EPITHELIAL CELLS.  
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN  
CC RECEPTOR SUBFAMILY.  
CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
DR EMBL, U57509; AAB05209.1; -;  
DR EMBL, X57240; CAA40516.1; -;  
DR PIR, S30502; S30502.  
DR HSSP, P00523; 2PTRK.  
DR MGD, MGI:99216; Ddrl.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR000421; FAS58\_C.  
DR InterPro: IPR002011; RTkinaseII.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam, PF00754; F5\_F8\_type\_C; 1.  
DR ProDom, PD000001; Euk\_pkinase; 1.  
DR SMART, SM00231; FAS58C; 1.  
DR SMART, SM00219; TYRC; 1.  
DR PROSITE, PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
DR PROSITE, PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE, PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE, PS00239; RECEPTOR\_TYR\_KIN\_II; 1.  
DR PROSITE, PS01285; FAS58C\_1; 1.  
DR PROSITE, PS01286; FAS58C\_2; 1.  
DR Transferrase; Tyrosine-protein kinase; Glycoprotein; Signal;  
KW Phosphorylation; Transmembrane; Receptor; ATP-binding;  
KW Alternative splicing.  
FT SIGNAL 1 19  
FT CHAIN 20 911  
FT DOMAIN 20 414  
FT POTENTIAL.  
FT EPIITHELIAL DISCOIDIN DOMAIN RECEPTOR 1.  
FT EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 415 441  
FT POTENTIAL.  
FT CYTOPLASMIC (POTENTIAL).  
FT F5/8 TYPE C (PHOSPHOLIPID-BINDING,  
FT DOMAIN 442 911  
FT POTENTIAL).  
FT 32 186  
FT DOMAIN 379 413  
FT GLY/PRO-RICH.  
FT DOMAIN 474 599  
FT GLY/PRO-RICH.  
FT NP\_BIND 608 903  
FT PROTEIN KINASE.  
FT BINDING 614 622  
FT ATP (BY SIMILARITY).  
FT ACT\_SITE 653 653  
FT ATP (BY SIMILARITY).  
FT ACT\_SITE 764 764  
FT BY SIMILARITY.  
FT DISULFID 32 186  
FT MOD\_RES 511 511  
FT BY SIMILARITY.  
FT MOD\_RES 790 790  
FT PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
FT MOD\_RES 794 794  
FT PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
FT MOD\_RES 795 795  
FT PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
FT CARBOHYD 213 213  
FT N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 262 262  
FT N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 372 372  
FT N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 392 392  
FT N-LINKED (GLCNAC...) (POTENTIAL).  
FT VARSPLIC 503 539  
FT MISSING (IN ISOFORM CAK II).  
SQ SEQUENCE 911 AA; 101160 MW; DBB7FE03DD79510 CRC64;  
Query Match 7.0%; Score 87; DB 1; Length 911;  
Best Local Similarity 24.5%; Pred. No. 10;  
Matches 38; Conservative 12; Mismatches 35; Indels 70; Gaps 9;  
QY 143 PWIRQNFSCRLCQCQPDSSITLP-PW---SPPLPATA-----PTAPQP----- 184  
Dy 357 PWLFFSELSFSD-VNDSDTFFPAPWPPPPFSSLELEPRGQGVAAAEPSPTA 415  
QY 185 -----PLLLILLPVGLLLAAACLHWOR---TRRR-----T 214  
Dy 416 ILICLVAIIILLILLITALLML---WRLHWRLLSKERRVLEBELTVHLSVPGDTLLN 471  
QY 215 PRGEQVPP-----VPSQDILL 232  
Dy 472 NRGPREFPYQEPFRGTPPHSAPCVNGSALL 506  
RESULT 11  
CNCG4\_BOVIN  
ID CNCG4\_BOVIN STANDARD; PRT; 1394 AA.  
AC Q281B1; Q28082; Q03861;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 240 kDa protein of rod photoreceptor CNCG-channel [contains: Glutamic  
DE acid-rich protein (GARP); Cyclic nucleotide-gated cation channel 4  
DE (CNG channel 4) (CNG-4) (Cyclic nucleotide-gated cation channel  
DE modulatory subunit)].  
GN CNGB1 OR CNCG4.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RP MEDLINE=96009859; PubMed=7546742;  
RX Koerschen H.G., Illing M., Seifert R., Sesti F., Williams A.,  
RX Getzes S., Colville C., Mueller F., Dose A., Godde M., Molday L.,  
RX Kaupp U.B., Molday R.S.;  
RT "A 240 kDa protein represents the complete beta subunit of the cyclic  
RT nucleotide-gated channel from rod photoreceptor."  
RL Neuron 15:627-636(1995).  
RN [2]  
RP SEQUENCE OF 454-1394 FROM N.A.  
RC TISSUE=Testis;  
RX MEDLINE=96198098; PubMed=8626431;  
RX Biel M., Zong X., Ludwig A., Sautter A., Hofmann F.;  
RT "Molecular cloning and expression of the modulatory subunit of the  
RT cyclic nucleotide-gated cation channel."  
RL J. Biol. Chem. 271:6349-6355(1996).





Query Match	6.8%;	Score 85;	DB 1;	Length 366;
Best Local Similarity	22.2%;	Pred. No. 5.2;		
Matches 51;	Conservative 21;	Mismatches 66;	Indels 92;	Gaps 11;

RESULT	15
ABF1_MOUSE	
ID	ABF1_MOUSE
STANDARD;	
PRT;	3726 AA.

DT 16-OCT-2001 (Rel. 40, last sequence update)  
 DT 16-OCT-2001 (Rel. 40, last annotation update)  
 DE Alpha-fetoprotein enhancer binding protein (An motif-binding factor)  
 DE (ATF-binding transcription factor 1).  
 GN ATF1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BA1B/MK x ICR; TISSUE=Brain;  
 MD MEDLINE=96194902; PubMed=8654949;  
 ID Ido A., Miura Y., Watanabe M., Sakai M., Inoue Y.,  
 RA Hashimoto T., Morinaga T., Nishi S., Tamaoki T.,  
 RA Miki T.,

RT	"Cloning of the cDNA encoding the mouse ATFb1 transcription factor.";
RL	Gene 168:227-231(1986).
CC	-1 FUNCTION: Transcriptional activator that binds to the AT-rich core
CC	sequence of the enhancer element of the AFP gene.
CC	-1 SUBCELLULAR LOCATION: Nuclear.
CC	-1 SIMILARITY: CONTAINS 4 HOMEBOX DOMAINS.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL; D26046; BAA05046.1; .
DR	HSSP; P20263; LOCp.
DR	TRANSFAC; T03881; .
DR	MED; MGI:99948; Atbf1.
DR	InterPro; IPR001356; Homeobox.
DR	InterPro; IPR000822; Znf_C2H2.
DR	InterPro; IPR003604; Znf_U1.
DR	Pfam; PF00046; homeobox; 4.
DR	Pfam; PF00096; zf-C2H2; 20.
DR	ProDom; PD000010; Homeobox; 4.
DR	SMART; SM00389; HOX; 4.
DR	SMART; SM00355; Znf_C2H2; 22.
DR	SMART; SM00451; Znf_U1; 7.
DR	PROSITE; PS00027; HOMEBOX_1; 2.
DR	PROSITE; PS50071; HOMEBOX_2; 4.
DR	PROSITE; PS00028; ZINC_FINGER_C2H2_1; 15.
DR	PROSITE; PS50157; ZINC_FINGER_C2H2_2; 9.
KW	Transcription regulation; Activator; Zinc-finger; Metal-binding;
KM	DNA-binding; Homeobox; Nuclear protein; Repeat.
FT	ZN_FING 79 103 C2H2-TYPE.
FT	ZN_FING 282 305 C2H2-TYPE.
FT	ZN_FING 641 664 C2H2-TYPE.
FT	ZN_FING 672 695 C2H2-TYPE.
FT	ZN_FING 727 751 C2H2-TYPE.
FT	ZN_FING 805 829 C2H2-TYPE. (ATYPICAL).
FT	ZN_FING 946 969 C2H2-TYPE (DEGENERATE).
FT	ZN_FING 985 1009 C2H2-TYPE (ATYPICAL).
FT	ZN_FING 1041 1065 C2H2-TYPE (ATYPICAL).
FT	ZN_FING 1089 1113 C2H2-TYPE (ATYPICAL).
FT	ZN_FING 1233 1256 C2H2-TYPE (ATYPICAL).
FT	ZN_FING 1262 1285 C2H2-TYPE.
FT	ZN_FING 1370 1395 C2H2-TYPE.
FT	ZN_FING 1411 1433 C2H2-TYPE.
FT	ZN_FING 1439 1462 C2H2-TYPE.
FT	ZN_FING 1535 1579 C2H2-TYPE.
FT	ZN_FING 1606 1630 C2H2-TYPE.
FT	ZN_FING 1990 2013 C2H2-TYPE.
FT	DNA_BIND 2152 2211 HOMEBOX 1.
FT	DNA_BIND 2249 2308 HOMEBOX 2.
FT	ZN_FING 2335 2358 C2H2-TYPE (ATYPICAL).
FT	ZN_FING 2539 2561 C2H2-TYPE.
FT	DNA_BIND 2650 2709 HOMEBOX 3.
FT	ZN_FING 2720 2743 C2H2-TYPE.
FT	DNA_BIND 2952 3011 HOMEBOX 4.
FT	ZN_FING 3032 3056 C2H2-TYPE.
FT	ZN_FING 3552 3576 C2H2-TYPE.
FT	DOMAIN 461 491 POLY-GLU.
FT	DOMAIN 771 785 POLY-ALA.
FT	DOMAIN 1314 1317 POLY-ALA.
FT	DOMAIN 1734 1748 POLY-GLN.
FT	DOMAIN 1794 1799 POLY-GLN.
FT	DOMAIN 1856 1863 POLY-GLN.
FT	DOMAIN 2044 2059 POLY-PRO.
FT	DOMAIN 2405 2408 POLY-ALA.
FT	DOMAIN 3216 3220 POLY-PRO.
FT	DOMAIN 3380 3409 POLY-GLN.
FT	DOMAIN 3412 3420 POLY-GLN.
FT	DOMAIN 3534 3550 POLY-GLY.

FT DOMAIN 3620 3623 POLY-PRO.  
FT DOMAIN 3659 3662 POLY-SER.  
SQ SEQUENCE 3726 AA; 406567 MW; 915ACBE588A72C98 CRC64;

Query Match 6.8%; Score 84.5; DB 1; Length 3726;  
Best local similarity 21.6%; Pred. No. 80;  
Matches 53; Conservative 29; Mismatches 70; Indels 93; Gaps 12;

QY 29 DCSFQHSPISSDFAVKIRELSDYLLQDYPPVTVASNLQDEE--LCGGLWRLVLAQRMERL 86  
DB 3033 ECTLCGIKYSARLSVRDHIFSQOHISKVMDTIGSQLDKKEKEYEDPATVROQLMAQQELDRI 3092  
QY 87 KTV-----AGSKMÖGL-----LERVNTETHEFTKCAFQ--PP-----PSCLERFVQTN 126  
DB 3093 KKAENEVLGLAAQQÖGQFDNAPLQALNLP--TTPALÖGIPVLLPGINRPSLPGFTPAN 3149  
QY 127 ISRLQETSEQLVALKPWITTRQNFSCRLELQÖQPDSSFTLPPW-----S 170  
DB 3150 TA-----LTSFRP-----NLMLGP-STIVPSGLPTSGLPNKPSASLSS 3188  
QY 171 PRPLENTAFTAPQÖPPLLLLLLPVGLLLAAMCLHWOTRRRTPRPGEOVPP----- 223  
DB 3189 PTPAQATMAMAPQPP-----PÖPQÖPQPPVQÖPPPPPAQÖ 3224  
QY 224 VPSPO 228  
DB 3225 IPAPQ 3229

Search completed: November 24, 2002, 10:10:39  
Job time : 12.573 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 24, 2002, 10:08:21 ; Search time 26.2232 Seconds

(without alignments)  
1846.499 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242  
Sequence: 1 MTVLAPAWSPTTYLLLL...RPGQVPVPSPQDLLVEH 235

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	895.5	72.1	294	6	Q9MZV0
2	894.5	72.0	291	6	Q9MZU9
3	840	67.6	292	6	Q9GKE0
4	835	67.2	292	6	Q8WNW1
5	746	60.1	274	6	Q9GKD9
6	602.5	48.5	172	11	Q61I04
7	578	46.5	169	11	Q8VCH4
8	112.5	9.1	579	10	Q91G68
9	104.5	8.4	668	5	Q9GTY11
10	102.5	8.3	648	5	Q9GY33
11	100.5	8.1	1809	11	Q8VIR6
12	98.5	7.9	345	5	Q9N753
13	95.5	7.7	1240	12	Q9DWH8
14	93.5	7.5	658	10	Q9C570
15	93	7.5	1217	5	Q17889
16	92.5	7.4	387	11	Q8VD70

17	92.5	7.4	560	5	Q9GYA1	Q9GYA1 leishmania
18	92.5	7.4	1400	5	Q8S2S7	Q8S2S7 drosophila
19	92	7.4	251	4	Q9HAD2	Q9HAD2 homo sapien
20	90.5	7.3	536	5	Q9GYA0	Q9GYA0 leishmania
21	90.5	7.3	660	5	Q9GY15	Q9GY15 leishmania
22	90.5	7.3	5120	13	Q9PU36	Q9PU36 gallus gall
23	89.5	7.2	474	5	Q17610	Q17610 caenorhabdi
24	88.5	7.1	238	16	Q8YWX3	Q8YWX3 anabaena sp
25	88.5	7.1	270	4	Q9UMT1	Q9UMT1 homo sapien
26	88.5	7.1	404	10	Q9AMJ4	Q9AMJ4 oryza sativ
27	88.5	7.1	1267	10	Q9A3D5	Q9A3D5 oryza sativ
28	88.5	7.1	1386	4	Q75064	Q75064 homo sapien
29	88	7.1	250	6	Q9GKE2	Q9GKE2 sus scrofa
30	88	7.1	675	11	Q9DBT2	Q9DBT2 mus musculus
31	88	7.1	753	12	Q56971	Q56971 kennedy ye
32	87.5	7.0	470	10	Q9LUI1	Q9LUI1 arabidopsis
33	87.5	7.0	946	10	Q22015	Q22015 cyllindrothe
34	87	7.0	510	5	Q44018	Q44018 leishmania
35	87	7.0	5317	5	Q8TA74	Q8TA74 hemientrot
36	86.5	7.0	299	6	Q9TTF9	Q9TTF9 bos taurus
37	86	6.9	255	11	Q9D3J3	Q9D3J3 mus musculus
38	86	6.9	299	12	Q84647	Q84647 paramacium
39	86	6.9	706	5	Q23600	Q23600 caenorhabdi
40	86	6.9	911	11	Q35407	Q35407 mus musculus
41	85.5	6.9	795	5	Q950Q2	Q950Q2 toxoplasma
42	85	6.8	282	4	Q9BSA1	Q9BSA1 homo sapien
43	85	6.8	289	16	Q9A3K1	Q9A3K1 caulobacter
44	85	6.8	413	11	Q99NM1	Q99NM1 mus musculus
45	85	6.8	1217	4	Q9P2D0	Q9P2D0 homo sapien

## ALIGNMENTS

### RESULT 1

Q9MZV0 ID Q9MZV0 PRELIMINARY; PRT; 294 AA.  
AC Q9MZV0;  
DT 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
DE Flt3 ligand.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_Taxid=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20358731; PubMed=10902925;  
RA Yang S., Sim G.K.;  
RT "Molecular cloning of canine and feline flt3 ligand reveals high  
RT degree of similarity to the human and mouse homologue but uniquely  
RT long cytoplasmic domain."  
RL DNA Seq. 11:163-166(2000).  
DR EMBL; AF15148; AAF87088.1; -  
DR InterPro; IPR004213; Flt3\_lig.  
DR Pfam; PFO2947; Flt3\_lig; 1.  
SQ SEQUENCE 294 AA; 32394 MW; 6859917A3B74ABCD CRC64;

Query Match 72.1%; Score 895.5; DB 6; Length 294;  
Best Local Similarity 77.1%; Pred. No. 3.5e-80;  
Matches 182; Conservative 12; Mismatches 35; Indels 7; Gaps 3;

QY 1 MTVLAPAWSPTTYLLLLSSGSGTQDCSFQHSPISSDFAVKIRLSYLLQDYPVY 60  
DB 1 MTVLAPAWSPTASLLLLSPGLGTPDCSFHSPISTFAVTKRLSDYLLQDYPVY 60  
QY ASNIQDERLCGILRWLVLAQRMERLKTVAAGSKMQLGLERYNTEIHFTVCARQPPSCL 120  
DB 61 ASNIQDDDLGAFWRVLAQRMWRRLQAVAGSQMQLLEAVNTEIHFTVCARQPPSCL 120  
QY 121 RFOVNTSRLLQETSEQLVALKPWITRONFSRCLQCCQPPDSSTLPPEWSRPLEATAPT 180  
||||||| |||:|:| |||||:|:| |||||:|:| |||||:|:| |||||:|:| |||||:|:|

[illegible]

## RESULT 2

ID	ORGANISM	PRELIMINARY	PRC	291	AA
AC	ORGANISM				
DT	01-OCT-2000 (TREMBLrel. 15, Created)				
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	Felis ligand.				
OS	Felis silvestris catus (Cat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.				
OX	NCBI_TaxID=9685;				

RP SEQUENCE FROM N.A.  
RX MEDLINE=20358731; PubMed=10902925;  
RA Yang S., Sim G.K.;  
RT "Molecular cloning of canine and feline *flt3* ligand reveals high  
RT degree of similarity to the human and mouse homologue but unique  
RT long cytoplasmic domain.";  
RL DNA Seq. 11:165-166(2000);  
DR EMBL: AF155149; AAF87089.1; -  
DR InterPro: IPR004213; Flt3\_11g.  
PR Pdam: PFO2947; Flt3\_31g.1.  
RQ SOURCE= 291 AA; 32459 MW; 8F85A10A5EA0DC6 CRC64;

Query Match	72.0%;	Score 894.5;	DB 6;	Length 291;
Best Local Similarity	80.5%;	Pred. No. 4.3e-80;		
Matches 178; Conservative	9;	Mismatches 33;	Indels 1;	Gaps 1

[illegible]

### RESULT 3

ID	Q9GKE0	PRELIMINARY;	PTT;	292 AA.
AC	Q9GKE0;			
DT	01-MAR-2001	(TREMBLrel. 16, Created)		
DT	01-MAR-2001	(TREMBLrel. 16, last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, last annotation update)		
DE	Flt3 ligand isoform-1.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovine; Bos.			
NC	NCBI_taxid=9913;			
NC	NCBI_taxid=9913			

RP SEQUENCE FROM N.A.  
RX MEDLINE=20570936; PubMed=11120823;  
RA Mwangi W., Brown W.C., Palmer G.H.;  
RT "Identification of fetal liver tyrosine kinase 3 (Flk3) ligand domain  
RT required for receptor binding and function using naturally occurring  
RT ligand isoforms.";

RT J. Immunol. 165:6966-6974 (2000).  
 DR EMBL, AF282985; AAF99322.1; -.  
 DR InterPro, IPR004213; FIt3\_11g.  
 DR Pfam, PF02947; FIt3\_11g; 1.  
 SQ SEQUENCE 292 AA: 32390 MW; D68B9ED79221202D CRC64

query match

[illegible]

## RESULT 4

ID	OBMMNI:	PRELIMINARY:	PRT;	292 AA.
AC	OBMMNI:			
DT	01-MAR-2002 (TREMBREL.	20.	Created)	
DT	01-MAR-2002 (TREMBREL.	20.	Last sequence update)	
DT	01-JUN-2002 (TREMBREL.	21.	Last annotation update)	
DE	Flt3 ligand.			
GN	FLT3 LIGAND.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxId=9913;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RA	Hikono H., Momotani E.;			
RT	"Cloning of a cDNA for bovine flt3 ligand."			
RL	Submitted (NOV-2000) to the EMBL/GenBank/DBD databases.			
DR	EMBL; AB051841; BAB9634.1;			
DR	Interp: IP004213; Flt3_19.			
DR	RefSeq: PF02947; flt3.3; I.			
QO	SEQUENCE 292 AA; 3238 MW; 2A797E0C1199C9D CRC64;			

## Query Match

Matches 170; Conservative 12; Mismatches 38; Indels 4; Gaps 2;

QY 1 MYLAAASPTT-YLLLLLLSSLSSTQCSQHPSPISSDAAVAKIRELSYLLQDPYV 59

Db 1 MYVLAASWSPPTSLLLLLLLSPSLQSTPPCSQRHSPISSTPAIKIGKLSYLLQDPYV 60

QY 60 VASNLQDELQCGILRLVLAORMMERLKTVAAGSKMGLLEPNTLEIHKVTCAPQPPSC 119

Db 61 VASNLQDDKLCAPWRLVLAORMMGRKLTVAAGSEMKLLLEDVNTLEIHKVTCAPQPLPSC 120

QY 120 LRFVQTNISRLQMTSEDLVAIKPMTIRONSFSCLELQCPDSTLPAPPMSRPLEATAP 179

Db 121 LRFVQANISHLQDTHQGLEAKRPWILHRNFSFSCLELQCPDSTPLLPFRPRGALGATSL 180

QY 180 TADPDP--LLILLIPYGLLLLAANACIHWQTRRRTRPGEQ 220

Db 181 PGQSFQSLLLLLLLIPALLLLATATAGCLCRMRRRRRRRTYPCR 224

## RESULT 5

## RESULT 5

```
Q9GKD9          PRELIMINARY;      PRT;      274 AA.
ID  Q9GKD9;
DT  01-MAR-2001 (Tremblrel. 16, Created)
DT  01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT  01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE  Flt3 ligand isoform-2.
OS  Bos taurus (Bovine).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC  Bovidae; Bovinae; Bos.
OX  NCBI_TaxID=9913;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=20570936; PubMed=11120823;
RA  Mwangi W., Brown W.C., Palmer G.H.;
RT  Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain
RT  required for receptor binding and function using naturally occurring
RT  ligand isoforms.
RL  J. Immunol. 165:6966-6974(2000).
DR  EMBL; AF282986; AAF93323.1; -.
DR  InterPro: IPR004213; Flt3_lig.
DR  Pfam: PF02947; flt3_lig; 1.
SQ  SEQUENCE 274 AA; 30372 MW; 725A7E77A95DA98B CRC64;

Query Match          60.1%; Score 746; DB 6; Length 274;
Best Local Similarity 69.6%; Pred. No. 1.8e-65;
Matches 156; Conservative 12; Mismatches 34; Indels 22; Gaps 3;

QY  1 MTVLAPAMSP--TYYLTLTLSSGSLGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPT 59
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  1 MTVLAPAMSPSTLTLTLTLSPGLGTQDCSFHSPISSTFAIKIGKLSKYLQDYPT 60

QY  60 VASNLQDEELCGLMRLVLAQRMMERLKTAVAGSKMOGLLEVRNTEIHFTVKCAFQPPSPC 119
    ||||||| :||| ||||||| ||||||| ||||||| :||| ||||||| |||||
Db  61 VASNLQDDKICGAFWRLVLAQRMMGRKLTAVAGSEMKLEEDVTEIHFTVTSCAF----- 114

QY  120 LRFVQTNISRLQETSEQVVALKPWITR--ONFSRCLELQCPDPSSTLP--PPWSRPRELTA 179
    || :|| ||||| :||| ||||||| ||||| ||||| ||||| ||||| |||||
Db  115 -----ODTHQOLEALKPWITHRNFSRCLELQCPDPSPTLLPPSPGALGATSL 162

QY  180 TAPQPP---TLTLTLTLSSGSLGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPT 220
    ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db  163 PGQSPLLTLTLTLTLTLTLTLATWACLCRWRRRRRTTRYPGR 206

RESULT 6
061104          PRELIMINARY;      PRT;      172 AA.
ID  061104;
AC  061104;
DT  01-NOV-1996 (Tremblrel. 01, Created)
DT  01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT  01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE  Flt3 ligand, fl169 form.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  McClanahan T., Culpepper J., Campbell D., Wagner J., Franz-Bacon K.,
RA  Mattson J., Tsai S., Luh J., Guimares M.J., Mattei M.-G., Rosnet O.,
RA  Birnbaum D., Hannum C.;
RT  Flt3 ligand: expression, genomic organization, alternatively spliced
RT  forms and processing.
RT  Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR  EMBL; U44024; AAA93305.1; -.
DR  MGD; MGI:95560; Flt3l.
DR  InterPro: IPR004213; Flt3_lig.
DR  InterPro: IPR001230; Prenyl_site.
DR  Pfam: PF02947; flt3_lig; 1.
DR  PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
```

```
SQ  SEQUENCE 172 AA; 19465 MW; 04F0A010171E3B84 CRC64;

Query Match          48.5%; Score 602.5; DB 11; Length 172;
Best Local Similarity 72.6%; Pred. No. 1.5e-51;
Matches 122; Conservative 15; Mismatches 28; Indels 3; Gaps 2;

QY  1 MTVLAPAMSP--TYYLTLTLSSGSLGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPT 59
    ||||||| :||| ||||||| ||||||| ||||||| :||| ||||||| |||||
Db  1 MTVLAPAMSPNSLLTLTLTLSPCLRGTPDCYFSHSPISNFKYKFRRLTDHLKDYPT 60

QY  60 VASNLQDEELCGLMRLVLAQRMMERLKTAVAGSKMOGLLEVRNTEIHFTVKCAFQPPSPC 119
    ||||| :||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db  61 VAVNLQDEKCKALMSFLAQRWIEQLKTAVAGSKMQLLEEDVTEIHFTVTSCTFQPLPEC 120

QY  120 LRFVQTNISRLQETSEQVVALKPWITR--ONFSRCLELQCPDPSSTLP--PPWSRPRELTA 172
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  121 LRFVQTNISHLKDPCTQLLAKPCIGKACQNFSCLE-----TPPCCPQ 166

RESULT 7
08VCH4          PRELIMINARY;      PRT;      169 AA.
ID  08VCH4;
AC  08VCH4;
DT  01-MAR-2002 (Tremblrel. 20, Created)
DT  01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT  01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE  Similar to FMS-like tyrosine kinase 3 ligand.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Strausberg R.;
RT  TISSUE=LIVER;
RA  Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC019801; AAI19801.1; -.
DR  InterPro: IPR004213; Flt3_lig.
DR  Pfam: PF02947; flt3_lig; 1.
SQ  SEQUENCE 169 AA; 18986 MW; 5B4CA47D9724EFP2 CRC64;

Query Match          46.5%; Score 578; DB 11; Length 169;
Best Local Similarity 68.6%; Pred. No. 3.7e-49;
Matches 120; Conservative 14; Mismatches 29; Indels 12; Gaps 3;

QY  1 MTVLAPAMSP--TYYLTLTLSSGSLGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPT 59
    ||||||| :||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db  1 MTVLAPAMSPNSLLTLTLTLSPCLRGTPDCYFSHSPISNFKYKFRRLTDHLKDYPT 60

QY  60 VASNLQDEELCGLMRLVLAQRMMERLKTAVAGSKMOGLLEVRNTEIHFTVKCAFQPPSPC 119
    ||||||| :||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db  61 VAVNLQDEKCKALMSFLAQRWIEQLKTAVAGSKMQLLEEDVTEIHFTVTSCTFQPLPEC 120

QY  120 LRFVQTNISRLQETSEQVVALKPWITR--ONFSRCLELQCPDPSSTLP--PPWSRPRELTA 172
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  121 LRFVQTNISHLKDPCTQLLAKPCIGKACQNFSCLE-----TPPCCPQ 166

RESULT 8
09LGG8          PRELIMINARY;      PRT;      579 AA.
ID  09LGG8;
AC  09LGG8;
DT  01-OCT-2000 (Tremblrel. 15, Created)
DT  01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT  01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE  Putative extensin-like protein.
OS  Oryza sativa (Rice).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC  Ehrhartoideae; Oryzaeae; Oryza.
OX  NCBI_TaxID=4530;
```



ID 08VIM6 PRELIMINARY: PRT: 1809 AA.  
 AC 08VIM6:  
 DT 01-MAR-2002 (TREMblrel. 20, Created)  
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Stereocillin.  
 GN STRC.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BAIB/C.  
 RX MEDLINE=21547528; PubMed=11687802.  
 RA Verly E., Masmoudi S., Zwaenepoel I., Leibovici M., Hutchin T.P.,  
 RA Del Castillo I., Nouaille S., Blanchard S., Laine S., Popot J.L.,  
 RA Moreau F., Mueller R.F., Petit C.;  
 RT "Mutations in a new gene encoding a protein of the hair bundle cause  
 RT non-syndromic deafness at the DFNB16 locus."  
 RL Nat. Genet. 29:345-349(2001).  
 DR EMBL: AF375593; AAL35321.1; -.  
 DR MGD: MGI:2153816; Strc.  
 SQ SEQUENCE 1809 AA; 196404 MW; 012382C9E80EC825 CRC64;

Query Match 8.1%; Score 100.5; DB 11; Length 1809;  
 Best Local Similarity 23.7%; Pred. No. 0.74;  
 Matches 70; Conservative 25; Mismatches 93; Indels 107; Gaps 14;

QY 3 VLAPAWSPPTVLL-----LLLL-----SSGLSGTQCSFQHSISSDFAVKIRE 47  
 DB 168 VLAADWLPLMLLESTRQALVOLQPSVDPYTNATGLD-----RE 208  
 48 LSDYLLQDY--PVYASNLQDEE-LOGGLMRLV---LAQRMNERIKTV----- 89  
 DB 209 PAVHFLQGLGLITPAGELGSEALWGLRTVGAPLYAAGLELLRYHSHQDEVFSIM 268  
 QY 90 -----AGSKMGLLERVNTETIEFYVKC-----AFQPPSCLEFVQTNISRL 131  
 DB 269 GQPEPDASGCGGNIQQLLWGMNRNLSWDARALGFLSGSPPPALHCLSRGVP--L 326  
 QY 132 QETSEOLVALKFWITRONFSRCLQLQCCDPSSTLP-----PMSPRPLE 175  
 DB 327 PRASQPAHAISP---RQRAISVEALCENHSGPEPPYSTISNFYLLCOHICAPPRPP 383  
 QY 176 AT--APTAPQPPPLLLLLLPGVLLLAAMWCIHQRTERRTPRGEQVP--PVPS 226  
 DB 384 TTPRPPTTPQPPPTTQIP-----DTTQPPPVTPRPPTTPQPPPS 426

RESULT 12  
 ID 09N753 PRELIMINARY: PRT: 345 AA.  
 AC 09N753:  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Probable surface antigen p2.  
 GN LM12.08.  
 OS Leishmania major.  
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
 OX NCBI\_TaxID=5664;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ERIEDLIN;  
 RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,  
 RA Oliver K.;  
 RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: AL390114; CAB98658.2; -.  
 DR InterPro: IPR001611; LRR.  
 DR Pfam: PF00560; LRR; 3.  
 DR SMART: SM00370; LRR; 3.

SO SEQUENCE 345 AA; 37530 MW; 06ECC850B1B54B70 CRC64;  
 Query Match 7.9%; Score 98.5; DB 5; Length 345;  
 Best Local Similarity 23.8%; Pred. No. 0.17;  
 Matches 56; Conservative 21; Mismatches 57; Indels 101; Gaps 10;

QY 6 PAMSEPTVLLLLLLSSGLST-----QDCSFQHSISSDFAVKIRELS 49  
 DB 152 PEMGSMSTSLVNLNRGIGISCTLPQWGMGSKARSLQLODCDLSGSPSSWSAI----- 205  
 QY 50 DYLLQDYVTVASNLQDEELG-----GLMRLVLAQRMNERIKTVGSKMGLLERVNT 104  
 DB 206 -----PMLASVSLKGNKFCGVCRTGIRLVLL--WTSSTRATA----- 245  
 QY 105 IHFYTKCAFQ--PPSCLREFVQTNISRLLOETSEOLVALKFWITRONFSRCLQCCPD 161  
 DB 246 --WLLRTVQGRPLPLPPRQRPRTSLT-----PPLRSGPR 278  
 QY 162 SSTLPSPSPPLPENTATPAPQPLLL-----LLPGVLLLAAMWCIHQRTRR 212  
 DB 279 LSRLPQALRRHRLN-----PQPLRRHRLNRPPLP-----QQTRR 313

RESULT 13  
 ID 09DWH8 PRELIMINARY: PRT: 1240 AA.  
 AC 09DWH8:  
 DT 01-MAR-2001 (TREMblrel. 16, Created)  
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Pr2.  
 GN R2.  
 OS Rat cytomegalovirus (strain Mastricht).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Betaherpesvirinae; Muromegalovirus.  
 OX NCBI\_TaxID=79700;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MASTRICHT;  
 RX MEDLINE=20366325; PubMed=10906222;  
 RA Vink C., Beuken E., Bruggeman C.A.;  
 RT "Complete DNA sequence of the rat cytomegalovirus genome."  
 RL J. Virol. 74:7656-7665(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MASTRICHT;  
 RX MEDLINE=20473137; PubMed=11018281;  
 RA Gruijthuisen Y.K., Beuken E., Bruggeman C.A., Vink C.;  
 RT "Rat cytomegalovirus R89 is a highly conserved gene which expresses a  
 RT spliced transcript."  
 RL Virus Res. 69:119-130(2000).  
 DR EMBL: AF332689; AAF99111.1; -.  
 SQ SEQUENCE 1240 AA; 125612 MW; 33B6C13DC6A272B0 CRC64;

Query Match 7.7%; Score 95.5; DB 12; Length 1240;  
 Best Local Similarity 33.0%; Pred. No. 1.5;  
 Matches 29; Conservative 8; Mismatches 18; Indels 33; Gaps 5;

QY 160 PDSSTL-----PPWSPRP--LWATAPAPQ--PLLLLLLPGVLLLA 201  
 DB 1060 PDSSTAYTGEATTRSPATPEPRPRPLPGVDSALPLAPQPTLLSLVPA----- 1112  
 QY 202 AMCLHMORTRRRTPRGEQVPPVPSPOD 229  
 DB 1113 -----QATRASRPETDAP--PTPAD 1132

RESULT 14  
 ID 09C5T0 PRELIMINARY: PRT: 658 AA.  
 AC 09C5T0:  
 DT 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 24, 2002, 10:02:26 ; Search time 31.7704 Seconds

(without alignments)  
985.632 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242  
Sequence: 1 MVLAPAWSPPTLYLLLLLL.....RPGQVPVPSFDLLVEH 235

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:\*  
2: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:\*  
3: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:\*  
4: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:\*  
5: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:\*  
6: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:\*  
7: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:\*  
8: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:\*  
9: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:\*  
10: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:\*  
11: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:\*  
12: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:\*  
13: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:\*  
14: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:\*  
15: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:\*  
16: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:\*  
17: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:\*  
18: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:\*  
19: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:\*  
20: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:\*  
21: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:\*  
22: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*  
23: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	16	AA67541 Human flt-3 ligand.
2	1242	100.0	235	20	AA67769 Human flt-3 ligand.
3	1242	100.0	235	21	AA69719 Full length wild t
4	1242	100.0	235	22	AA69719 Human flt-3 ligand
5	1242	100.0	235	23	AA69719 Human flt-3 ligand
6	1236	99.5	235	16	AA66175 Human S86/S109 Flt
7	1236	99.5	235	22	AA620194 Human flt-3 ligand
8	1124	89.7	209	19	AA69721 Human flt-3 mteint
9	1114	89.7	209	19	AA69721 Human flt-3 mteint
10	1114	89.7	209	21	AA69720 Mature wild type h

11	1110	89.4	209	21	AA69723 Human flt-3 mteint
12	1110	89.4	209	21	AA69726 Human flt-3 mteint
13	1110	89.4	209	21	AA69727 Human flt-3 mteint
14	1110	89.4	209	21	AA69729 Human flt-3 mteint
15	1108	89.2	209	21	AA69722 Human flt-3 mteint
16	1108	89.2	209	21	AA69724 Human flt-3 mteint
17	1107	89.1	209	21	AA69728 Human flt-3 mteint
18	1107	88.6	209	21	AA69725 Human flt-3 mteint
19	970	78.1	185	22	AA620195 Human flt-3 ligand
20	895.5	72.1	291	21	AA58204 Canine flt-3 ligand
21	894.5	72.0	291	21	AA58212 Canine flt-3 ligand
22	834	67.1	178	22	AA620193 Human flt-3 ligand
23	797.5	64.2	268	21	AA58205 Canine mature flt-
24	796.5	64.1	276	21	AA58207 Canine flt-3 ligand
25	791.5	63.7	265	21	AA58211 Canine mature flt-
26	768.5	61.9	231	16	AA67540 Mouse flt-3 ligand
27	768.5	61.9	231	20	AA67768 Murine flt-3 ligand
28	768.5	61.9	231	22	AA620186 Mouse flt-3 ligand
29	768	61.8	232	16	AA66177 Mouse M0110/7118
30	764	61.5	232	16	AA620189 Mouse flt-3 ligand
31	745	60.0	150	19	AAW7930 Flt3 ligand FLR10C
32	745	60.0	150	19	AAW69054 Human flt-3 recept
33	740.5	59.6	377	19	AAW78124 Chimeric receptor
34	739	59.5	143	19	AAW7926 Flt3 ligand FLR3C
35	739	59.5	143	19	AAW69050 Human flt-3 recept
36	737.5	59.4	349	19	AAW83289 Human flt-3 ligand
37	737.5	59.4	349	19	AAW87805 Flt3L 1-139/1962b/
38	736.5	59.3	340	19	AAW63291 Human flt-3 ligand
39	736.5	59.3	349	19	AAW83286 Human flt-3 ligand
40	736.5	59.3	523	19	AAW78008 Trimeric flt-3-G-C
41	735	59.2	140	19	AAW7911 Human flt-3 ligand
42	735	59.2	140	19	AAW69035 Human flt-3 recept
43	735	59.2	144	19	AAW7928 Flt3 ligand FLR4C
44	735	59.2	144	19	AAW69052 Human flt-3 recept
45	735	59.2	313	19	AAW83294 Human flt-3 ligand

#### ALIGNMENTS

RESULT 1	AA67541	standard; Protein: 235 AA.
ID	AA67541	
XX	AA67541	
AC	AA67541	
XX	AA67541	
DT	05-AUG-1995	(first entry)
DE	Human flt-3 ligand.	
XX	Human flt-3 ligand.	
XX	Human flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy.	
KW	Human flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy.	
OS	Homo sapiens.	
XX	Homo sapiens.	
FT	Key	Location/Qualifiers
FT	Peptide	1..26
FT	/label= Sig-peptide	/label= "signal peptide may extend to position 27"
FT	/note= "signal peptide may extend to position 27"	
FT	Domain	27..182
FT	/label= Extracellular-domain	/label= "extracellular domain may start at position 28"
FT	/note= "extracellular domain may start at position 28"	
FT	Domain	183..205
FT	/label= Transmembrane-domain	/label= "Transmembrane-domain
FT	Domain	206..235
FT	/label= Cytoplasmic-domain	/label= "Cytoplasmic-domain
PN	EP627487-A.	
XX	EP627487-A.	
XX	07-DEC-1994.	
PD	07-DEC-1994.	
XX	07-DEC-1994.	
PF	19-MAY-1994;	94EP-0303575.
XX	19-MAY-1994;	94EP-0303575.
XX	19-MAY-1994;	94EP-0303575.

PR 24-MAY-1993; 93US-0068394.  
 PR 12-AUG-1993; 93US-0106463.  
 PR 25-AUG-1993; 93US-0111758.  
 PR 03-DEC-1993; 93US-0162407.  
 PR 07-MAR-1994; 94US-0209502.  
 PR 11-MAY-1994; 94US-0243545.  
 XX  
 PA (IMMUNEX ) IMMUNEX CORP.  
 XX  
 PI Beckmann MP, Lyman SD;  
 XX  
 DR WPI: 1995-008071/02.  
 DR N-PSDB; AAQ79079.  
 XX  
 PT Isolated ligands for flt 3 receptors - useful for treating  
 PT anaemia, AIDS and various cancers  
 XX  
 PS Disclosure; Page 29-30; 33pp; English.  
 XX  
 CC A human T-cell lambda-gli0 random primed cDNA library was  
 CC screened with a fragment corresponding to the extracellular  
 CC domain of mouse flt3 ligand (flt3-L) (nt 103-516 of AAQ79076)  
 CC to isolate human flt3-L cDNA. Flt-3 stimulates progenitor and  
 CC stem cells, and can be used e.g. in gene therapy protocols.  
 XX  
 SQ Sequence 235 AA;  
 Query Match 100.0%; Score 1242; DB 16; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 5e-109;  
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MTVALPAMSPPTTYLLLLSSGLSGTQDCSFQHSPISSDPAVKIRELSYLLQDYPTV 60  
 DB 1 MTVALPAMSPPTTYLLLLSSGLSGTQDCSFQHSPISSDPAVKIRELSYLLQDYPTV 60  
 QY 61 ASNLQDEBELCGGLMRLVLAQRMERLKTVAAGSKQGLLERVNTETIHFTVCAEQPPSCL 120  
 DB 61 ASNLQDEBELCGGLMRLVLAQRMERLKTVAAGSKQGLLERVNTETIHFTVCAEQPPSCL 120  
 QY 121 RFVQTNISRLQETSEQVLALKPWITRONFSRCLELQCCPDSSSTLPSPSPRPLEATAPT 180  
 DB 121 RFVQTNISRLQETSEQVLALKPWITRONFSRCLELQCCPDSSSTLPSPSPRPLEATAPT 180  
 QY 181 APQPPLLILLPLVGLLLAAAWCLHMORTRRTPRPGEGVPPVPSPODLLVEH 235  
 DB 181 APQPPLLILLPLVGLLLAAAWCLHMORTRRTPRPGEGVPPVPSPODLLVEH 235  
 RESULT 2  
 AAW67769  
 ID AAW67769 standard; Protein; 235 AA.  
 AC  
 AC AAW67769;  
 XX  
 DT 25-MAR-1999 (first entry)  
 XX  
 DE Human flt3-L ligand.  
 XX  
 KW Antigen-specific peripheral immune tolerance; flt3-L ligand; flt3-L;  
 KW immunogenic; autoimmune disease; organ transplantation; food allergy;  
 KW tissue transplantation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9657655-A1.  
 PD 23-DEC-1998.  
 XX  
 PF 12-JUN-1998; 98WO-US12085.  
 XX  
 PR 17-JUN-1997; 97US-0877421.  
 XX  
 PA (IMMUNEX ) IMMUNEX CORP.

XX  
 PI Abboett NM, Mowat AM, Viney JL;  
 XX  
 DR WPI: 1999-070422/06.  
 DR N-PSDB; AAV81506.  
 XX  
 PT Methods for initiating or enhancing antigen specific immune  
 PT tolerance - by using murine or human flt3 ligand  
 XX  
 PS Claim 1; Page 14-15; 25pp; English.  
 XX  
 CC A method has been developed of initiating or enhancing: (i) an antigen-  
 CC specific immune tolerance; or (ii) immunotolerance of a therapeutic  
 CC immunogenic molecule by addition of a polypeptide, before, after or with  
 CC the mucosal administration of an immunotolerising amount of the antigen  
 CC or therapeutic molecule, respectively. The polypeptide is capable of  
 CC binding the flt3 receptor and is: a) amino acids 28-x of murine flt3  
 CC ligand (flt3-L), where x is an amino acid between 163-231; b) amino  
 CC acids 28-y of human flt3-L, where y is an amino acid between 160-235;  
 CC and c) a polypeptide that has at least 90% identity to the polypeptides  
 CC of either (a) or (b). The method ameliorates the effects of autoimmune  
 CC diseases, food allergies or organ or tissue rejection following  
 CC transplantation. Administration of flt3-L allows lower doses of antigens  
 CC to be used in vivo for mucosally administered antigens. The present  
 CC sequence represents human flt3-L.  
 XX  
 SQ Sequence 235 AA;  
 Query Match 100.0%; Score 1242; DB 20; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 5e-109;  
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MTVALPAMSPPTTYLLLLSSGLSGTQDCSFQHSPISSDPAVKIRELSYLLQDYPTV 60  
 DB 1 MTVALPAMSPPTTYLLLLSSGLSGTQDCSFQHSPISSDPAVKIRELSYLLQDYPTV 60  
 QY 61 ASNLQDEBELCGGLMRLVLAQRMERLKTVAAGSKQGLLERVNTETIHFTVCAEQPPSCL 120  
 DB 61 ASNLQDEBELCGGLMRLVLAQRMERLKTVAAGSKQGLLERVNTETIHFTVCAEQPPSCL 120  
 QY 121 RFVQTNISRLQETSEQVLALKPWITRONFSRCLELQCCPDSSSTLPSPSPRPLEATAPT 180  
 DB 121 RFVQTNISRLQETSEQVLALKPWITRONFSRCLELQCCPDSSSTLPSPSPRPLEATAPT 180  
 QY 181 APQPPLLILLPLVGLLLAAAWCLHMORTRRTPRPGEGVPPVPSPODLLVEH 235  
 DB 181 APQPPLLILLPLVGLLLAAAWCLHMORTRRTPRPGEGVPPVPSPODLLVEH 235  
 RESULT 3  
 AAY69719  
 ID AAY69719 standard; Protein; 235 AA.  
 AC  
 AC AAY69719;  
 XX  
 DT 05-JUL-2000 (first entry)  
 XX  
 DE Full length wild type human flt-3 protein.  
 XX  
 KW Immunomodulator; immunosuppressive; cytostatic; anti-anemic; anti-HIV;  
 KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;  
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;  
 KW cellular expansion; cellular differentiation; natural killer cell;  
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;  
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;  
 KW multiple myeloma; leukemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200001823-A2.  
 PD 13-JAN-2000.  
 XX



PF 25-JUN-1999; 99WO-US14296.  
XX  
PR 02-JUL-1998; 98US-0109100.  
XX  
PA (IMMUNEX CORP.  
XX  
PI Graddis TJ, McGrew JT;  
XX  
DR WPI: 2000-182115/16.  
XX  
N-PSDB; AAF59064.  
PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,  
PT immune response stimulation or treatment of pathological conditions  
PR contains amino acid substitutions at positions 8, 84, 118 or 122  
XX  
PS Claim 1; Page 72-73; 90pp; English.  
XX  
PS  
CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides  
CC which exhibits increased or decreased biological activity relative to  
CC the full length wild type (this sequence) or mature (AA169120). flt3-L  
CC polypeptides. The flt3-L protein binds cell surface tyrosine kinase  
CC receptors and regulate growth and differentiation of hematopoietic  
CC progenitor cells. The flt3-L protein can be used to induce cellular  
CC expansion (especially in vivo) or differentiation, e.g. in  
CC hematopoietic, natural killer (NK) or dendritic cells, especially in the  
CC presence of growth factors such as interleukins, colony stimulating  
CC factors or protein kinases. The protein can also modulate, augment or  
CC enhance a patient's immune response and can be used to treat an immune  
CC disorder (e.g. allergy, autoimmunity or immunosuppression). The protein  
CC may be used to treat a pathological condition e.g. myelodysplasia,  
CC aplastic anemia, HIV infection, breast, small cell lung, testicular or  
CC ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute  
CC leukemia.  
XX  
XX  
SQ Sequence 235 AA;  
Query Match 100.0%; Score 1242; DB 21; Length 235;  
Best Local Similarity 100.0%; Pred. No. 5e-109;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLDYPYTV 60  
DB 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLDYPYTV 60  
QY 61 ASNLDEELCGGLMRLVLAQRMERLKTVAAGSKMGGLELRVNTLHFYTKCAFQPPPSCL 120  
DB 61 ASNLDEELCGGLMRLVLAQRMERLKTVAAGSKMGGLELRVNTLHFYTKCAFQPPPSCL 120  
QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLCCQPPDSSTLPPWSPRPLEATAPT 180  
DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLCCQPPDSSTLPPWSPRPLEATAPT 180  
QY 181 AFQPLLLLLLPVGLLLAAAWCLHMORTRRTPRGEQVPPVPSDILLVHH 235  
DB 181 AFQPLLLLLLPVGLLLAAAWCLHMORTRRTPRGEQVPPVPSDILLVHH 235  
RESULT 4  
AAB20192  
ID AAB20192 standard; Protein; 235 AA.  
XX  
AC AAB20192;  
XX  
DT 14-MAY-2001 (first entry)  
XX  
DE Human Flt-3 ligand.  
XX  
KM Flt-3 ligand; fms-like tyrosine kinase; human; vaccine;  
KM immunotherapy; therapy; tumour; cancer; melanoma; glioma;  
KM lymphoma; autoimmune disease; infection; gene therapy.  
XX  
OS Homo sapiens.  
XX

FH Key Location/Qualifiers  
FT Peptide 1..26  
FT /label= Signal\_peptide  
FT Protein 27..235  
FT /label= Mature\_protein  
FT Domain 27..182  
FT /label= Extracellular\_domain  
FT Domain 183..205  
FT /label= Transmembrane\_domain  
FT Domain 206..235  
FT /label= Cytoplasmic\_domain  
PN WO200109303-A2.  
XX  
PD 08-FEB-2001.  
XX  
PF 31-JUL-2000; 2000WO-US20679.  
XX  
PR 30-JUL-1999; 99US-0146170.  
XX  
PA (VICA-) VICAL INC.  
XX  
PI Hermanson GG;  
XX  
DR WPI: 2001-123319/13.  
DR N-PSDB; AAF30310.  
XX  
CC The present sequence is that of human Fms-like tyrosine kinase  
CC (Flt-3 ligand). The invention is directed to enhancing the  
CC immune response of a vertebrate to an antigen or a cytokine by  
CC administering in vivo, into a tissue of a vertebrate, a Flt-3  
CC ligand-encoding polynucleotide, and 1 or more antigen- or  
CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding  
CC polynucleotide may encode the present full-length human Flt-3  
CC ligand polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185,  
CC or 27-235 of the ligand. The polynucleotides are incorporated  
CC into the cells of the vertebrate in vivo, and a prophylactically  
CC or therapeutically effective amount of Flt-3 ligand and 1 or more  
CC antigens or cytokines is produced in vivo. Pharmaceutical  
CC compositions comprising the polynucleotides are useful for  
CC suppressing tumour growth in a mammal. The tumour is melanoma,  
CC glioma or lymphoma, particularly B-cell lymphoma. They can also  
CC be used for the prophylactic and/or therapeutic treatment of:  
CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B  
CC and C in humans), parasitic (e.g. malaria) and fungal infections;  
CC (b) autoimmune diseases (e.g. rheumatoid arthritis and  
CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.  
CC Various other examples of these diseases are given in the  
CC specification.  
XX  
XX  
SQ Sequence 235 AA;  
Query Match 100.0%; Score 1242; DB 22; Length 235;  
Best Local Similarity 100.0%; Pred. No. 5e-109;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLDYPYTV 60  
DB 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLDYPYTV 60  
QY 61 ASNLDEELCGGLMRLVLAQRMERLKTVAAGSKMGGLELRVNTLHFYTKCAFQPPPSCL 120  
DB 61 ASNLDEELCGGLMRLVLAQRMERLKTVAAGSKMGGLELRVNTLHFYTKCAFQPPPSCL 120  
QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLCCQPPDSSTLPPWSPRPLEATAPT 180  
DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLCCQPPDSSTLPPWSPRPLEATAPT 180

Db 121 RFVQTNISRLLOETSEQLVALKPWITTRQNFSCLELOCQPDSSSTLPPWSPRPLEATAPT 180

QY 181 APQPELLLLLLPVGLLLAAAWCLHMQRTTRPRRGEQVPPVPSQDILLVEH 235  
 |||||

Db 181 APQPELLLLLLPVGLLLAAAWCLHMQRTTRPRRGEQVPPVPSQDILLVEH 235

RESULT 5

ABR08129

ID ABR08129 standard; protein; 235 AA.

XX

AC ABR08129;

DT 10-SEP-2002 (first entry)

XX

DE Human Flt3L polypeptide.

XX

KW Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial;  
 KW fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV;  
 KW tuberculostatic; cytostatic; human; Flt3L.

OS Homo sapiens.

XX

PN WO00236141-A2.

XX

PD 10-MAY-2002.

XX

PF 30-OCT-2001; 2001WO-US44834.

XX

PR 02-NOV-2000; 2000US-245721P.

XX

PA (IMMV ) IMMUNEX CORP.

XX

PI Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE;  
 PI Thomas EK;

XX

DR WPI; 2002-500114/53.

XX

PT Treating an individual suffering from infection, e.g. inflammation,  
 PT chickenpox or AIDS, by administering a combination of dendritic cell  
 PT mobilization factor or maturation agent, T cell enhancing factor and  
 PT antigen-specific T cells -

XX

PS Disclosure; Page 37-38; 43pp; English.

XX

CC The invention relates to treating an individual at risk for or suffering  
 CC from infection with a pathogenic or opportunistic organism. The method  
 CC involves administering a combination of two to five agents comprising:  
 CC (a) dendritic cell mobilisation factor; (b) dendritic cell maturation  
 CC agent; (c) dendritic cell activation agent; (d) T cell enhancing factor;  
 CC or (e) activated, antigen-specific T cells. The methods are useful for  
 CC treating an individual at risk for or suffering from infection with a  
 CC pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria  
 CC (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g.  
 CC T. cruzi, which causes Chaga's disease). The methods are especially  
 CC useful for treating an individual suffering from immunosuppression by  
 CC enhancing a lymphocyte-mediated immune response. In particular, the  
 CC method is useful for treating inflammations, chickenpox, oral or genital  
 CC herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS,  
 CC T cell leukemia or T cell lymphoma. The activated antigen-presenting  
 CC dendritic cells are useful as a vaccine adjuvant. The present sequence  
 CC represents a human Flt3L polypeptide fragment, that can be used as a  
 CC dendritic cell mobilisation factor.

XX

SQ Sequence 235 AA;

Query Match 100.0%; Score 1242; DB 23; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 5e-109;  
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYTAAWMSPTTYLLLLLSGLSTGQCFSQHSPISSDFAVKIRELSDYLLQDPYIV 60  
 |||||

Db 1 MYTAAWMSPTTYLLLLLSGLSTGQCFSQHSPISSDFAVKIRELSDYLLQDPYIV 60

QY 61 ASNLODEELCGGLNRLVLAQRMERLKTVAGSKMQGLLERVNTIEHFVTKCAFQPPPSCL 120  
 |||||

Db 61 ASNLODEELCGGLNRLVLAQRMERLKTVAGSKMQGLLERVNTIEHFVTKCAFQPPPSCL 120

QY 121 RFVQTNISRLLOETSEQLVALKPWITTRQNFSCLELOCQPDSSSTLPPWSPRPLEATAPT 180  
 |||||

Db 121 RFVQTNISRLLOETSEQLVALKPWITTRQNFSCLELOCQPDSSSTLPPWSPRPLEATAPT 180

QY 181 APQPELLLLLLPVGLLLAAAWCLHMQRTTRPRRGEQVPPVPSQDILLVEH 235  
 |||||

Db 181 APQPELLLLLLPVGLLLAAAWCLHMQRTTRPRRGEQVPPVPSQDILLVEH 235

RESULT 6

AAR66175

ID AAR66175 standard; Peptide; 235 AA.

XX

AC AAR66175;

DT 10-AUG-1995 (first entry)

XX

DE Human S86/S109 Flt3 ligand peptide sequence.

XX

KW Flt3 ligand; tyrosine kinase receptor ligand.

XX

OS Homo sapiens.

XX

PN WO9426891-A.

XX

PD 24-NOV-1994.

XX

PF 18-MAY-1994; 94WO-US05150.

XX

PR 19-MAY-1993; 93US-0065231.

PR 07-JUL-1993; 93US-0089263.

PR 16-JUL-1993; 93US-0092549.

PR 13-AUG-1993; 93US-0106340.

PR 24-AUG-1993; 93US-0112391.

PR 19-NOV-1993; 93US-0155111.

PR 03-DEC-1993; 93US-0162413.

XX

PA (INRM ) INST NAT SANTE & RECH MEDICALE.

XX

PS (SCHE ) SCHERING CORP.

XX

PI Birnbaum D, Culpepper JA, Hannum CH, Lee FD;

XX

DR WPI; 1995-006787/01.

XX

PT New ligand for the Flt3 tyrosine kinase receptor - and related  
 PT nucleic acid, vectors, host cells and antibodies, useful for  
 PT treating abnormal cell physiology and proliferation, e.g. cancer,  
 PT also for diagnosis and drug screening

XX

PS Claim 11; Page 76-77; 90pp; English.

XX

CC A cDNA library from the human stromal cell line 293SV48, in  
 CC pMT8, was screened with an 800 bp fragment derived from  
 CC mouse clone T118. This fragment encompasses the coding region  
 CC conserved between two mouse clones, T118 and T110. Approx. 20  
 CC positive clones were selected and partially sequenced. Two  
 CC clones, S86 and S109, were found to be approx. 75% homologous  
 CC to the mouse clones over the first 163 AAs. Clone S86 continued  
 CC to show homology to T110 until the stop codon, although to a  
 CC lesser degree, for an overall homology of 66%. Clones T118 and  
 CC S109 do not show homology to each other or to the other clones  
 CC after mouse residue 163 (human residue 160). An additiona mouse  
 CC clone designated M88 has a 29 AA insert at the junction between  
 CC the common and divergent portions of the mouse ligand.

XX

SQ Sequence 235 AA;

immune response of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a Flt-3 ligand-encoding polynucleotide, and 1 or more antigen- or cytokine-encoding polynucleotides. The Flt-3 ligand-encoding polynucleotide may encode the present full-length human Flt-3 ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-235 of the Flt-3 ligand. The polynucleotides are incorporated into the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of Flt-3 ligand and 1 or more antigens or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, glioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of: (a) bacterial (e.g. *Bacillus* infections), viral (e.g. hepatitis B and C in humans), parasitic (e.g. malaria) and fungal infections; (b) autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs. Various other

SQ Sequence 235 AA;

Query Match	99.58;	Score 1236;	DB 22;	Length 235;
Best Local Similarity	99.68;	Pred. No. 1.8e-108;		
Matches 234;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0

61 ASNLQDEELGALWRLVLAQRNMERLKTIVAGSKMQGLLERVNTETIHEVTKCAFQPPPSCL 120

121 REVONTNISP.IJEMSENOI VAI KBITPONESCI EI OODDESMI DDECEDDV E,E,DE 100

Db	QY
121	181
REVGQINISRLQETSEQLVALKPWITQNSRCLTEIQCPDSTLPPMSPRPLEATAPT	APQPLLLLLLVGSLLLAAACSLHMQTRRRTPRPGQVPPVPSPODLLVEH
181	181
APQPLLLLLLVGSLLLAAACSLHMQTRRRTPRPGQVPPVPSPODLLVEH	APQPLLLLLLVGSLLLAAACSLHMQTRRRTPRPGQVPPVPSPODLLVEH
181	181
APQPLLLLLLVGSLLLAAACSLHMQTRRRTPRPGQVPPVPSPODLLVEH	APQPLLLLLLVGSLLLAAACSLHMQTRRRTPRPGQVPPVPSPODLLVEH

RESULT 8	
AAV69721	
ID	AAV69721 standard; Protein; 212 AA

05-JUL-2000 (first entry)

Human flt-3 mutein L-3H.

immunomodulator; immunosuppressive; cytostatic; anti-HIV; anti-neoplastic; antiallergic; anti-anemic; anti-HIV; neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell

cancer; dendritic cell; immune response; autoimmunity; immunosuppression

multiple myeloma; leukemia; mutein.

13-JAN-2000.  
W0200001823-A2.

25-JUN-1999: 99W0-TIS14296

02-JUL-1998; 98US-0109100.

PA (IMMUNEX CORP.  
XX  
PI Graddis TJ, McGrew JT;  
XX  
DR WPI; 2000-182115/16.  
XX  
XX  
PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,  
PT immune response stimulation or treatment of pathological conditions  
PT contains amino acid substitutions at positions 8, 84, 118 or 122 -  
XX  
PS Claim 4; Page 79-80; 90pp; English.  
XX  
XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides  
CC which exhibits increased or decreased biological activity relative to  
CC the full length wild type (AA69720) or mature (AA69720) flt3-L  
CC polypeptides. This sequence represents an example of the novel flt3-  
CC ligands and comprises the L-3H mutant polypeptide. The flt3-L protein  
CC binds cell surface tyrosine kinase receptors and regulate growth and  
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can  
CC be used to induce cellular expansion (especially in vivo) or  
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic  
CC cells, especially in the presence of growth factors such as interleukins,  
CC colony stimulating factors or protein kinases. The protein can also  
CC modulate, augment or enhance a patient's immune response and can be used  
CC to treat an immune disorder (e.g. allergy, autoimmunity or  
CC immunosuppression). The protein may be used to treat a pathological  
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,  
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple  
CC myeloma, neuroblastoma or acute leukemia.  
XX  
XX Sequence 212 AA:  
SQ  
Query Match 90.5%; Score 1124; DB 21; Length 212;  
Best Local Similarity 100.0%; Pred. No. 5.9e-98;  
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 25 SGTDCSFQHSPISSDPAFAVKIRELSYLLQDYPVTVAASNLQDELCGGLMRVLAAQRMME 84  
DB 2 SGTDCSFQHSPISSDPAFAVKIRELSYLLQDYPVTVAASNLQDELCGGLMRVLAAQRMME 61  
QY 85 RLKTVAAGSKMOGLLEHVNTEIHFTVCARQPPSCLEFVQTNISRLQETSEQLVALKPMW 144  
DB 62 RLKTVAAGSKMOGLLEHVNTEIHFTVCARQPPSCLEFVQTNISRLQETSEQLVALKPMW 121  
QY 145 ITRQNSRCLCLEOCQPDSSSTLPPWMSRPLEATAPAPQPLLILLPVGLLLAAAMC 204  
DB 122 ITRQNSRCLCLEOCQPDSSSTLPPWMSRPLEATAPAPQPLLILLPVGLLLAAAMC 181  
QY 205 LHMQRTRRRTPRGEQVPVPSPODLLVEH 235  
DB 182 LHMQRTRRRTPRGEQVPVPSPODLLVEH 212  
RESULT 9  
AA69007  
ID AA69007 standard; peptide; 209 AA.  
XX  
AC AAM69007;  
XX  
DT 01-OCT-1998 (first entry)  
XX  
DE Human flt-3 receptor agonist.  
XX  
XX Human; flt-3 receptor agonist; haematopoietic cell stimulation; cancer;  
KM bone marrow reconstitution; haematological disease; immune deficiency;  
KM drug-induced myelosuppression; renal dialysis; gene therapy; infection;  
KM congenital metabolic disease; neurological disease; therapy;  
KM dendritic cell production.  
XX  
XX Homo sapiens.  
OS  
XX  
XX  
PN WO9818923-A1.  
XX

PD 07-MAY-1998.  
XX  
XX 23-OCT-1997; 97MC-US18700.  
XX  
XX 25-OCT-1996; 96US-0030094.  
XX  
XX (SEAR ) SEARLE & CC G D.  
PA  
XX  
XX Feng Y, McKearn JF, McWhorter CA, Minnerly JC, Munster NI;  
PI Staten NR, Streeter PR, Woulfe SL;  
XX  
XX WPI; 1998-272218/24.  
DR  
XX  
XX Rearranged flt-3 receptor agonists and nucleic acids encoding them -  
PT used to stimulate production of haematopoietic and dendritic cells,  
PT for treatment of hematological diseases, bone marrow reconstitution  
PT and in gene therapy  
XX  
XX Disclosure; Page 9-10; 158pp; English.  
CC This sequence represents a rearranged human flt-3 receptor agonists of  
CC the invention. The agonists have a modified flt-3 ligand amino acid  
CC sequence. The agonists are used to stimulate production of haematopoietic  
CC cells in vivo (e.g. in a subject about to donate blood) or for ex vivo  
CC expansion for subsequent transplantation, e.g. to reconstitute bone  
CC marrow after chemotherapy, disease etc., or to treat haematological  
CC disease such as drug-induced myelosuppression, defects caused by  
CC infections, burns or renal dialysis. Optionally ex vivo expanded cells  
CC are transduced with a gene therapy vector for treating e.g. congenital  
CC metabolic diseases, immune deficiency, neurological disease, cancer and  
CC infections. The agonists can also be used in the treatment of tumours,  
CC infections and autoimmune disease, when administered optionally with an  
CC antigen. The agonist can also be used in the production of dendritic  
CC cells for use as an immunising adjuvant for treatment disorders including  
CC acquired immune deficiency syndrome. Compared with native ligands, the  
CC new agonists have better stimulatory activity, reduced side effects  
CC and/or better physical properties such as solubility, stability or refold  
CC efficiency. When used together with other stimulatory agents, the  
CC agonists provide a synergistic effect.  
XX  
XX Sequence 209 AA:  
SQ  
Query Match 89.7%; Score 1114; DB 19; Length 209;  
Best Local Similarity 100.0%; Pred. No. 5.1e-97;  
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 27 TQDCSFQHSPISSDPAFAVKIRELSYLLQDYPVTVAASNLQDELCGGLMRVLAAQRMME 86  
DB 1 TQDCSFQHSPISSDPAFAVKIRELSYLLQDYPVTVAASNLQDELCGGLMRVLAAQRMME 60  
QY 87 KTVAGSKMOGLLEHVNTEIHFTVCARQPPSCLEFVQTNISRLQETSEQLVALKPMW 146  
DB 61 KTVAGSKMOGLLEHVNTEIHFTVCARQPPSCLEFVQTNISRLQETSEQLVALKPMW 120  
QY 147 RQNSRCLCLEOCQPDSSSTLPPWMSRPLEATAPAPQPLLILLPVGLLLAAAMC 206  
DB 121 RQNSRCLCLEOCQPDSSSTLPPWMSRPLEATAPAPQPLLILLPVGLLLAAAMC 180  
QY 207 WQTRRRTPRGEQVPVPSPODLLVEH 235  
DB 181 WQTRRRTPRGEQVPVPSPODLLVEH 209  
RESULT 10  
AA69720  
ID AA69720 standard; Protein; 209 AA.  
XX  
XX AAY69720;  
XX  
XX 05-JUL-2000 (first entry)  
DT  
XX  
XX Mature wild type human flt-3 protein.  
DE  
XX

Query Match	89.7%	Score 1114	DB 21	Length 209
Best Local Similarity	100.0%	Pred. No. 5.1e-97		
Matches 209	Conservative 0	Mismatches 0	Indels 0	Gaps 0
XX	Sequence	209 AA:		
OS	Homo sapiens.			
XX				
PN	WO200001823-A2.			
PD				
XX				
XX	13-JAN-2000.			
XX				
PF	25-JUN-1999; 99WO-US14296.			
PR				
XX	02-JUL-1998; 98US-0109100.			
XX				
PA	(IMMV ) IMMUNEX CORP.			
PI				
XX	Graddis TJ, McGrew JT;			
XX				
DR	WPI, 2000-182115/16.			
XX				
XX	N-PSDB; AA259064.			
XX				
PT	Mutant soluble flt3 ligand polypeptide used in cellular expansion,			
PT	immune response stimulation or treatment of pathological conditions			
XX	contains amino acid substitutions at positions 8, 84, 118 or 122			
XX				
PS	Claim 1: Page 89-90; 90pp; English.			
XX				
CC	The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides			
CC	which exhibits increased or decreased biological activity relative to			
CC	the full length wild type (AA699719) or mature (this sequence) flt3-L			
CC	polypeptides. The flt3-L protein binds cell surface tyrosine kinase			
CC	receptors and regulate growth and differentiation of hematopoietic			
CC	progenitor cells. The flt3-L protein can be used to induce cellular			
CC	expansion (especially in vivo) or differentiation, e.g. in			
CC	hematopoietic, natural killer (NK) or dendritic cells, especially in the			
CC	presence of growth factors such as interleukin, colony stimulating			
CC	factors or protein kinases. The protein can also modulate, augment or			
CC	enhance a patient's immune response and can be used to treat an immune			
CC	disorder (e.g. allergy, autoimmunity or immunosuppression). The protein			
CC	may be used to treat a pathological condition e.g. myelodysplasia,			
CC	aplastic anemia, HIV infection, breast, small cell lung, testicular or			
CC	ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute			
XX	leukemia.			
XX				
SO	Sequence	209 AA:		
Yy	Query Match	89.7%	Score 1114	DB 21
Db	Best Local Similarity	100.0%	Pred. No. 5.1e-97	Length 209
Yy	Matches 209	Conservative 0	Mismatches 0	Indels 0
Db				Gaps 0
Yy	27 TDGDFHSHSPSSDPAVKVIRELSDVLDDPYTVASNIQDEELCGMLRVLAQRMERL 86			
Db	1 TDGDFHSHSPSSDPAVKVIRELSDVLDDPYTVASNIQDEELCGMLRVLAQRMERL 60			
Yy	87 KTVAGSKMQGLERNTIEHFTVKCAFQPPPCSLFVYOTNISRLQENFSEQVVALKPMRT 146			
Db	61 KTVAGSKMQGLERNTIEHFTVKCAFQPPPCSLFVYOTNISRLQENFSEQVVALKPMRT 120			
Yy	147 RQNSRCLFELCCOPDSSITLPPWSPRPLEATAPAPQPLLLLLLVGLLLAAACIH 206			
Db	121 RQNSRCLFELCCOPDSSITLPPWSPRPLEATAPAPQPLLLLLLVGLLLAAACIH 180			
Yy	207 WQTRRRRTPRGEGVPPVPSFODLLLVH 235			
Db	181 WQTRRRRTPRGEGVPPVPSFODLLLVH 209			

ID	AA69723 standard; Protein; 209 AA.
XX	
AC	AA69723;
XX	
DT	05-JUL-2000 (first entry)
XX	
DE	Human flt-3 mutein K84E.
XX	
KW	Immunomodulator; immunosuppressive; cytostatic; antileukemic; anti-HIV;
KW	neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
KW	cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW	cellular expansion; cellular differentiation; natural killer cell;
KW	cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW	myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW	multiple myeloma; leukemia; mutein.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200001823-A2.
XX	
PD	13-JAN-2000.
XX	
PF	25-JUN-1999; 99WO-US14296.
XX	
PR	02-JUL-1998; 98US-0109100.
XX	
PA	(IMMUNEX CORP.
XX	
PI	Graddis TJ; McGrew JT;
XX	
DR	WPI; 2000-182115/16.
XX	
PT	Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT	immune response stimulation or treatment of pathological conditions
PT	contains amino acid substitutions at positions 8, 84, 118 or 122 -
PS	Claim 4; Page 84-85; 90pp; English.
XX	
CC	The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC	which exhibits increased or decreased biological activity relative to
CC	the full length wild type (AA69719) or mature (AA69720) flt3-L
CC	polypeptides. This sequence represents an example of the novel flt-3
CC	ligands and comprises the K84E mutant polypeptide. The flt3-L protein
CC	binds cell surface tyrosine kinase receptors and regulate growth and
CC	differentiation of hematopoietic progenitor cells. The flt3-L protein can
CC	be used to induce cellular expansion (especially in vivo) or
CC	differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC	cells, especially in the presence of growth factors such as interleukins,
CC	colony stimulating factors or protein kinases. The protein can also
CC	modulate, augment or enhance a patient's immune response and can be used
CC	to treat an immune disorder (e.g. allergy, autoimmunity or
CC	immunosuppression). The protein may be used to treat a pathological
CC	condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC	small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC	myeloma, neuroblastoma or acute leukemia.
XX	
SO	Sequence 209 AA;
XX	
Query Match	89.4%; Score 1110; DB 21; Length 209;
Best Local Similarity	99.5%; Pred. No. 1,2e-96;
Matches 208; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	27 TQDCSFQHSIISDFAVKIRELSLDYLDQPYTVASNIQDEELCGGIMRLVLAQRMERL 86
Db	1 TQDCSFQHSIISDFAVKIRELSLDYLDQPYTVASNIQDEELCGGIMRLVLAQRMERL 60
QY	87 KTVAGSKMQILERVNTEIHFVTKCAFOPPSPSCLEFVOTNISRLOETSEQVAKPMIT 146
Db	61 KTVAGSKMQILERVNTEIHFVTECAFOPPSPSCLEFVOTNISRLOETSEQVAKPMIT 120
QY	147 KQNFRCLELQCDSSSTLPPWSPPELAVTAQPPPLLLLLLPVGLLLAAAWCLH 206
Db	1 KQNFRCLELQCDSSSTLPPWSPPELAVTAQPPPLLLLLLPVGLLLAAAWCLH 206

DB 121 RQNFSCLELQCCPDSSLPPEPWSRPLEATAPAPQPELILLLLPVGLLLAAACGLH 180

QY 207 WQTRRRTRPRGEGVPPVPSPODLLVEH 235  
 |||||

DB 181 WQTRRRTRPRGEGVPPVPSPODLLVEH 209

RESULT 12  
 AAY69726  
 ID AAY69726 standard; Protein; 209 AA.

AC AAY69726;  
 XX  
 DT 05-JUL-2000 (first entry)

DE Human flt-3 muteln Q122R.  
 XX  
 XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;  
 KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;  
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;  
 KW cellular expansion; cellular differentiation; natural killer cell;  
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;  
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;  
 KW multiple myeloma; leukemia; muteln.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200001823-A2.  
 XX  
 PD 13-JAN-2000.  
 XX  
 PE 25-JUN-1999; 99WO-US14296.  
 PR 02-JUL-1998; 98US-0109100.  
 XX  
 XX (IMMV ) IMMUNEX CORP.  
 PA  
 PI Graddis TJ, McGrew JT;  
 XX  
 DR WPI; 2000-182115/16.  
 XX  
 PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,  
 PT immune response stimulation or treatment of pathological conditions  
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -  
 XX  
 PS Claim 4; Page 88-89; 90pp; English.  
 XX  
 CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides  
 CC which exhibits increased or decreased biological activity relative to  
 CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L  
 CC polypeptides. This sequence represents an example of the novel flt-3  
 CC ligands and comprises the Q122R mutant polypeptide. The flt3-L protein  
 CC binds cell surface tyrosine kinase receptors and regulate growth and  
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can  
 CC be used to induce cellular expansion (especially in vivo) or  
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic  
 CC cells, especially in the presence of growth factors such as interleukins,  
 CC colony stimulating factors or protein kinases. The protein can also  
 CC modulate, augment or enhance a patient's immune response and can be used  
 CC to treat an immune disorder (e.g. allergy, autoimmunity or  
 CC immunosuppression). The protein may be used to treat a pathological  
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,  
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple  
 CC myeloma, neuroblastoma or acute leukemia.  
 CC  
 XX  
 SQ Sequence 209 AA;  
 Query Match 89.4%; Score 1110; DB 21; Length 209;  
 Best Local Similarity 99.5%; Pred. No. 1.2e-96;  
 Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 121 RQNFSCLELQCCPDSSLPPEPWSRPLEATAPAPQPELILLLLPVGLLLAAACGLH 180

QY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCRLRYVQINISLQETSQVALAKPWIT 146  
 |||||

DB 61 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCRLRYVQINISLQETSQVALAKPWIT 120

QY 147 RQNFSCLELQCCPDSSLPPEPWSRPLEATAPAPQPELILLLLPVGLLLAAACGLH 206  
 |||||

DB 121 RQNFSCLELQCCPDSSLPPEPWSRPLEATAPAPQPELILLLLPVGLLLAAACGLH 180

QY 207 WQTRRRTRPRGEGVPPVPSPODLLVEH 235  
 |||||

DB 181 WQTRRRTRPRGEGVPPVPSPODLLVEH 209

RESULT 13  
 AAY69727  
 ID AAY69727 standard; Protein; 209 AA.

AC AAY69727;  
 XX  
 DT 05-JUL-2000 (first entry)

DE Human flt-3 muteln L26F.  
 XX  
 XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;  
 KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;  
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;  
 KW cellular expansion; cellular differentiation; natural killer cell;  
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;  
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;  
 KW multiple myeloma; leukemia; muteln.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200001823-A2.  
 XX  
 PD 13-JAN-2000.  
 XX  
 PE 25-JUN-1999; 99WO-US14296.  
 PR 02-JUL-1998; 98US-0109100.  
 XX  
 XX (IMMV ) IMMUNEX CORP.  
 PA  
 PI Graddis TJ, McGrew JT;  
 XX  
 DR WPI; 2000-182115/16.  
 XX  
 PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,  
 PT immune response stimulation or treatment of pathological conditions  
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -  
 XX  
 PS Claim 13; Page 82-83; 90pp; English.  
 XX  
 CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides  
 CC which exhibits increased or decreased biological activity relative to  
 CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L  
 CC polypeptides. This sequence represents an example of the novel flt-3  
 CC ligands and comprises the L26F mutant polypeptide. The flt3-L protein  
 CC binds cell surface tyrosine kinase receptors and regulate growth and  
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can  
 CC be used to induce cellular expansion (especially in vivo) or  
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic  
 CC cells, especially in the presence of growth factors such as interleukins,  
 CC colony stimulating factors or protein kinases. The protein can also  
 CC modulate, augment or enhance a patient's immune response and can be used  
 CC to treat an immune disorder (e.g. allergy, autoimmunity or  
 CC immunosuppression). The protein may be used to treat a pathological  
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,  
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple

CC myeloma, neuroblastoma or acute leukemia.  
 XX  
 SQ Sequence 209 AA;  
 Query Match 89.4%; Score 1110; DB 21; Length 209;  
 Best Local Similarity 99.5%; Pred. No. 1.2e-96;  
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 27 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPTVASNLODEELCGGLMRVLAAQRMERL 86  
 DB 1 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPTVASNLODEELCGGLMRVLAAQRMERL 60  
 QY 87 KTVAGSKMOGLERVNTETHEFTKCAFOPPPSCLRFVQTNISRLLOETSEQLVALKPWIT 146  
 DB 61 KTVAGSKMOGLERVNTETHEFTKCAFOPPPSCLRFVQTNISRLLOETSEQLVALKPWIT 120  
 QY 147 RQNSRCLLELQCCPDSSITLPPMSPRPLEATAPAPQPPILLLLPVGILLAAACGLH 206  
 DB 121 RQNSRCLLELQCCPDSSITLPPMSPRPLEATAPAPQPPILLLLPVGILLAAACGLH 180  
 QY 207 WQTRRRTRPRGEGVPPVPSPODLLLVEH 235  
 DB 181 WQTRRRTRPRGEGVPPVPSPODLLLVEH 209

## RESULT 14

AA69729  
 ID AAY69729 standard; Protein: 209 AA.  
 XX  
 AC AAY69729;  
 XX  
 DT 05-JUL-2000 (first entry)  
 XX  
 DE Human flt-3 mutein A64T.

XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;  
 KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;  
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;  
 KW cellular expansion; cellular differentiation; natural killer cell;  
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;  
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;  
 KW multiple myeloma; leukemia; mutein.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 PN WO200001823-A2.  
 XX  
 PD 13-JAN-2000.  
 XX  
 PD 25-JUN-1999; 99WO-US14296.  
 PF  
 XX 02-JUL-1998; 98US-0109100.  
 PR  
 XX (IMMV ) IMMUNEX CORP.  
 PA  
 XX Graddis TJ, McGrew JT;  
 XX  
 DR WPI: 2000-182115/16.  
 XX  
 PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,  
 PT immune response stimulation or treatment of pathological conditions  
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -  
 XX  
 PS Claim 13; Page 78-79; 90pp; English.  
 XX

CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides  
 CC which exhibits increased or decreased biological activity relative to  
 CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L  
 CC polypeptides. This sequence represents an example of the novel flt3-L  
 CC ligands and comprises the 126F mutant polypeptide. The flt3-L protein  
 CC binds cell surface tyrosine kinase receptors and regulate growth and  
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can

CC be used to induce cellular expansion (especially in vivo) or  
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic  
 CC cells, especially in the presence of growth factors such as interleukins,  
 CC colony stimulating factors or protein kinases. The protein can also  
 CC modulate, augment or enhance a patient's immune response and can be used  
 CC to treat an immune disorder (e.g. allergy, autoimmunity or  
 CC immunosuppression). The protein may be used to treat a pathological  
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,  
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple  
 CC myeloma, neuroblastoma or acute leukemia.  
 CC  
 XX

## SQ Sequence 209 AA;

Query Match 89.4%; Score 1110; DB 21; Length 209;  
 Best Local Similarity 99.5%; Pred. No. 1.2e-96;  
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 27 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPTVASNLODEELCGGLMRVLAAQRMERL 86  
 DB 1 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPTVASNLODEELCGGLMRVLAAQRMERL 60  
 QY 87 KTVAGSKMOGLERVNTETHEFTKCAFOPPPSCLRFVQTNISRLLOETSEQLVALKPWIT 146  
 DB 61 KTVAGSKMOGLERVNTETHEFTKCAFOPPPSCLRFVQTNISRLLOETSEQLVALKPWIT 120  
 QY 147 RQNSRCLLELQCCPDSSITLPPMSPRPLEATAPAPQPPILLLLPVGILLAAACGLH 206  
 DB 121 RQNSRCLLELQCCPDSSITLPPMSPRPLEATAPAPQPPILLLLPVGILLAAACGLH 180  
 QY 207 WQTRRRTRPRGEGVPPVPSPODLLLVEH 235  
 DB 181 WQTRRRTRPRGEGVPPVPSPODLLLVEH 209

## RESULT 15

AA69722  
 ID AAY69722 standard; Protein: 209 AA.  
 XX  
 AC AAY69722;  
 XX  
 DT 05-JUL-2000 (first entry)  
 XX  
 DE Human flt-3 mutein H8Y.

XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;  
 KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;  
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;  
 KW cellular expansion; cellular differentiation; natural killer cell;  
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;  
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;  
 KW multiple myeloma; leukemia; mutein.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 PN WO200001823-A2.  
 XX  
 PD 13-JAN-2000.  
 XX  
 PD 25-JUN-1999; 99WO-US14296.  
 PF  
 XX 02-JUL-1998; 98US-0109100.  
 PR  
 XX (IMMV ) IMMUNEX CORP.  
 PA  
 XX Graddis TJ, McGrew JT;  
 XX  
 DR WPI: 2000-182115/16.  
 XX  
 PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,  
 PT immune response stimulation or treatment of pathological conditions  
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -  
 XX

PS Claim 4; Page 81-82; 90pp; English.

The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AAV69719) or mature (AAV69720) flt3-L polypeptides. This sequence represents an example of the novel flt-3 ligands and comprises the 887 mutant polypeptide. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoietic progenitor cells. The flt3-L protein can be used to induce cellular expansion (especially in vivo) or differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, colony stimulating factors or protein kinases. The protein can also modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or immunosuppression). The protein may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, small cell lung, testicular or ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute leukemia.

SQ Sequence 209 AA;

Query Match	Score	DB	Length
89.2%	1108	21	209

Best Local Similarity 99.5%; Pred. No. 1.9e-96;  
 Matches 308; Conservation 1; Mismatches 0

Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	27	TOUSFOHSPISSPFAKIRELSYLLQDPVIVASNLQDEBJCGIMRLVLAORWNERL	86
Db	1	TODSFQSPSSPFAKIRELSYLLQDPVIVASNLQDEBJCGIMRLVLAORWNERL	60
QY	87	KTVAGSKMOGLLEBYENTEIHFVTKCAQCPSPCLRFVOTNISRLQETSBDLALKWMT	146
Db	61	KTVAGSKMOGLLEBYENTEIHFVTKCAQCPSPCLRFVOTNISRLQETSBDLALKWMT	120
QY	147	RONFSRCLELQCPDSSSTFLPPWSPRPLEATAPPAQDPBLLLLLVGYLLLLAAACGH	206
Db	121	RONFSRCLELQCPDSSSTFLPPWSPRPLEATAPPAQDPBLLLLLVGYLLLLAAACGH	180
QY	207	WORTFRRTPRGEOVPVPSPODLLLVEN	235
Db	181	WORTFRRTPRGEOVPVPSPODLLLVEN	209

Search completed: November 24, 2002, 10:10:12  
Job time : 32.7704 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 24, 2002, 10:11:46 ; Search time 8.57296 Seconds

(without alignments)  
429,309 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242

Sequence: 1 MTVLAPAWSPRTYLLLLLL.....RFGQVPPVSPQDLLVEH 235

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications-AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	9	US-10-095-449-6
2	1242	100.0	235	10	US-09-448-378-1
3	1242	100.0	235	10	US-09-983-806-6
4	1242	100.0	235	10	US-09-904-536-1
5	1124	90.5	212	10	US-09-904-536-18
6	1114	89.7	209	10	US-09-904-536-10
7	1110	89.4	209	10	US-09-904-536-9
8	1110	89.4	209	10	US-09-904-536-12
9	1110	89.4	209	10	US-09-904-536-14
10	1110	89.4	209	10	US-09-904-536-17
11	1108	88.2	209	10	US-09-904-536-11
12	1108	88.2	209	10	US-09-904-536-15
13	1107	88.1	209	10	US-09-904-536-13
14	1106	88.0	209	10	US-09-904-536-16
15	1100	86.6	209	10	US-10-095-449-2
16	768.5	61.9	231	9	US-09-448-378-2
17	768.5	61.9	231	10	US-09-983-806-2
18	768.5	61.9	231	10	US-09-983-806-1
19	506.5	40.8	137	10	US-09-904-536-19

20	91.5	7.4	674	10	US-09-899-471-2	Sequence 2, Appl
21	91.5	7.4	698	10	US-09-899-471-5	Sequence 5, Appl
22	89.5	7.2	874	10	US-09-826-508-26	Sequence 26, Appl
23	89.5	7.2	941	9	US-09-793-139-47	Sequence 47, Appl
24	89.5	7.2	941	10	US-09-818-879-47	Sequence 47, Appl
25	89.5	7.2	941	10	US-09-211-7558-47	Sequence 47, Appl
26	87.5	7.0	415	10	US-09-826-212-6	Sequence 47, Appl
27	87.5	7.0	415	10	US-09-907-372-20	Sequence 20, Appl
28	87.5	7.0	415	10	US-09-935-727-8	Sequence 8, Appl
29	87.5	7.0	479	9	US-10-108-605-57	Sequence 57, Appl
30	87.5	7.0	570	9	US-09-991-496-104	Sequence 104, App
31	87.5	7.0	570	10	US-09-874-923-104	Sequence 104, App
32	85.5	6.9	519	10	US-09-925-300-1680	Sequence 1680, Ap
33	84.5	6.8	610	10	US-09-783-708-1	Sequence 1, Appl
34	84.5	6.8	913	10	US-09-223-490-4	Sequence 4, Appl
35	84.5	6.8	1134	9	US-10-001-873-50	Sequence 50, Appl
36	84	6.8	107	10	US-09-220-920-52	Sequence 24, Appl
37	84	6.8	220	10	US-09-220-920-26	Sequence 26, Appl
38	84	6.8	220	10	US-09-804-615-9	Sequence 9, Appl
39	84	6.8	1252	9	US-10-047-542-89	Sequence 89, Appl
40	82.5	6.6	334	10	US-09-953-342-24	Sequence 24, Appl
41	81.5	6.6	488	10	US-09-801-196-26	Sequence 26, Appl
42	81.5	6.6	865	9	US-09-957-995A-19	Sequence 19, Appl
43	81	6.5	428	9	US-10-047-542-60	Sequence 60, Appl
44	81	6.5	428	10	US-09-916-230-1	Sequence 1, Appl
45	81	6.5	574	9	US-10-047-542-45	Sequence 45, Appl

## ALIGNMENTS

RESULT 1  
US-10-095-449-6  
Sequence 6, Application US/10095449  
Patent No. US20020160004A1  
GENERAL INFORMATION:  
APPLICANT: Lyman, Stewart D.  
Beckmann, M. Patricia  
TITLE OF INVENTION: Ligands for f1c3/flk-2 Receptors  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.0.1  
SOFTWARE: Microsoft Word, Version #5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/095,449  
FILING DATE: 13-Mar-2002  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/669,692  
FILING DATE: 24-JUN-1996  
APPLICATION NUMBER: US/08/162,407  
FILING DATE: December 3, 1993  
APPLICATION NUMBER: 08/111,758  
FILING DATE: August 25, 1993  
APPLICATION NUMBER: 08/106,463  
FILING DATE: August 12, 1993  
APPLICATION NUMBER: 08/068,394  
FILING DATE: May 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2813-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-095-449-6

Query Match 100.0%; Score 1242; DB 9; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-103;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLILLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTVY 60  
DB 1 MTVALPAMSPPTTYLLILLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTVY 60  
QY 61 ASNLQDEELCGGLMRVLVAQRMMERLKTAVGSKMOGLLEERVNTEIHFTVKCAFPQPPSCL 120  
DB 61 ASNLQDEELCGGLMRVLVAQRMMERLKTAVGSKMOGLLEERVNTEIHFTVKCAFPQPPSCL 120  
QY 121 RFVQTNISRLQETSEQVALKPMWTRONFSRCLELQCCPDSTLPPWSPRPLEATAPT 180  
DB 121 RFVQTNISRLQETSEQVALKPMWTRONFSRCLELQCCPDSTLPPWSPRPLEATAPT 180  
QY 121 RFVQTNISRLQETSEQVALKPMWTRONFSRCLELQCCPDSTLPPWSPRPLEATAPT 180  
DB 121 RFVQTNISRLQETSEQVALKPMWTRONFSRCLELQCCPDSTLPPWSPRPLEATAPT 180  
QY 181 APOPELLLLLLPVGLLLAAAMCLHWQTRRRTPRREGVPPVPSQDILLVEH 235  
DB 181 APOPELLLLLLPVGLLLAAAMCLHWQTRRRTPRREGVPPVPSQDILLVEH 235

## RESULT 2

US-09-448-378-1  
Sequence 1, Application US/09448378  
Patent No. US20020034517A1  
GENERAL INFORMATION:  
APPLICANT: Brasel, Kenneth  
TITLE OF INVENTION: Dendritic Cell Stimulatory Factor  
FILE REFERENCE: 2836-D  
CURRENT APPLICATION NUMBER: US/09/448,378  
CURRENT FILING DATE: 1999-11-23  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: Patent version 3.0  
SEQ ID NO 1  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-448-378-1

Query Match 100.0%; Score 1242; DB 10; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-103;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLILLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTVY 60  
DB 1 MTVALPAMSPPTTYLLILLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTVY 60  
QY 61 ASNLQDEELCGGLMRVLVAQRMMERLKTAVGSKMOGLLEERVNTEIHFTVKCAFPQPPSCL 120  
DB 61 ASNLQDEELCGGLMRVLVAQRMMERLKTAVGSKMOGLLEERVNTEIHFTVKCAFPQPPSCL 120  
QY 121 RFVQTNISRLQETSEQVALKPMWTRONFSRCLELQCCPDSTLPPWSPRPLEATAPT 180  
DB 121 RFVQTNISRLQETSEQVALKPMWTRONFSRCLELQCCPDSTLPPWSPRPLEATAPT 180  
QY 181 APOPELLLLLLPVGLLLAAAMCLHWQTRRRTPRREGVPPVPSQDILLVEH 235  
DB 181 APOPELLLLLLPVGLLLAAAMCLHWQTRRRTPRREGVPPVPSQDILLVEH 235

## RESULT 3

US-09-983-806-6

Sequence 6, Application US/09983806  
Patent No. US20020107365A1  
GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.  
Beckmann, M. Patricia  
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.0.1  
SOFTWARE: Microsoft Word, Version #5.1

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/983,806  
FILING DATE: 25-Oct-2001  
CLASSIFICATION: 530

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/444,626  
FILING DATE: 19-MAY-1995  
APPLICATION NUMBER: US 08/162,407  
FILING DATE: 03-DEC-1993  
APPLICATION NUMBER: 08/111,758  
FILING DATE: August 25, 1993  
APPLICATION NUMBER: 08/106,463  
FILING DATE: August 12, 1993  
APPLICATION NUMBER: 08/068,394  
FILING DATE: May 24, 1993

## ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2813-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644

## INFORMATION FOR SEQ ID NO: 6:

## SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-983-806-6

Query Match 100.0%; Score 1242; DB 10; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-103;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLILLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTVY 60  
DB 1 MTVALPAMSPPTTYLLILLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTVY 60  
QY 61 ASNLQDEELCGGLMRVLVAQRMMERLKTAVGSKMOGLLEERVNTEIHFTVKCAFPQPPSCL 120  
DB 61 ASNLQDEELCGGLMRVLVAQRMMERLKTAVGSKMOGLLEERVNTEIHFTVKCAFPQPPSCL 120  
QY 121 RFVQTNISRLQETSEQVALKPMWTRONFSRCLELQCCPDSTLPPWSPRPLEATAPT 180  
DB 121 RFVQTNISRLQETSEQVALKPMWTRONFSRCLELQCCPDSTLPPWSPRPLEATAPT 180  
QY 181 APOPELLLLLLPVGLLLAAAMCLHWQTRRRTPRREGVPPVPSQDILLVEH 235  
DB 181 APOPELLLLLLPVGLLLAAAMCLHWQTRRRTPRREGVPPVPSQDILLVEH 235

## RESULT 4

US-09-904-536-1  
; Sequence 1, Application US/09904536  
; Patent No. US20020111475A1  
; GENERAL INFORMATION:  
; APPLICANT: Gradidis, Thomas J.  
; APPLICANT: McGrew, Jeffrey T.  
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
; FILE REFERENCE: 03260.0028  
; CURRENT APPLICATION NUMBER: US/09/904,536  
; CURRENT FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100  
; PRIOR FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-904-536-1

Query Match 100.0%; Score 1242; DB 10; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-103;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALAPAMSPFTYLLDLLLSGLSGTODCSFQHSPISSDFAVKIRELSYLLQDYPVY 60  
DB 1 MTVALAPAMSPFTYLLDLLLSGLSGTODCSFQHSPISSDFAVKIRELSYLLQDYPVY 60  
QY 61 ASNIQDEELCGGLMRVLVLAQRMMERLKTVAAGSKQGLLEVRNTEIHFTVKCAFQPPSCL 120  
DB 61 ASNIQDEELCGGLMRVLVLAQRMMERLKTVAAGSKQGLLEVRNTEIHFTVKCAFQPPSCL 120  
QY 121 RFOVNTNLSRLQETSSEQVVALKFWITRONFSRCLELQCGDSSSTLPPWSPRLEATAP 180  
DB 121 RFOVNTNLSRLQETSSEQVVALKFWITRONFSRCLELQCGDSSSTLPPWSPRLEATAP 180  
QY 181 APOPELLELLLVGLLLAAACLIHQWTRRRTPRPGEOVPPVPSPODLLVEH 235  
DB 181 APOPELLELLLVGLLLAAACLIHQWTRRRTPRPGEOVPPVPSPODLLVEH 235

RESULT 5  
US-09-904-536-10  
; Sequence 10, Application US/09904536  
; Patent No. US20020111475A1  
; GENERAL INFORMATION:  
; APPLICANT: Gradidis, Thomas J.  
; APPLICANT: McGrew, Jeffrey T.  
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
; FILE REFERENCE: 03260.0028  
; CURRENT APPLICATION NUMBER: US/09/904,536  
; CURRENT FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100  
; PRIOR FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 212  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-904-536-10

Query Match 90.5%; Score 1124; DB 10; Length 212;  
Best Local Similarity 100.0%; Pred. No. 5.4e-93;  
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 SGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVYASNIQDEELCGGLMRVLVLAQRMM 84  
DB 2 SGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVYASNIQDEELCGGLMRVLVLAQRMM 84  
QY 85 RLKTVAAGSKQGLLEVRNTEIHFTVKCAFQPPSCLRFVQTNISRLQETSSEQVVALKFW 144  
DB 85 RLKTVAAGSKQGLLEVRNTEIHFTVKCAFQPPSCLRFVQTNISRLQETSSEQVVALKFW 144

QY 145 ITRQNFSCLELQCGDSSSTLPPWSPRLEATAPAPOPPLLLLVGLLLAAAC 204  
DB 122 ITRQNFSCLELQCGDSSSTLPPWSPRLEATAPAPOPPLLLLVGLLLAAAC 181  
QY 205 LHMQRTRRRTPRPGEOVPPVPSPODLLVEH 235  
DB 182 LHMQRTRRRTPRPGEOVPPVPSPODLLVEH 212

RESULT 6  
US-09-904-536-18  
; Sequence 18, Application US/09904536  
; Patent No. US20020111475A1  
; GENERAL INFORMATION:  
; APPLICANT: Gradidis, Thomas J.  
; APPLICANT: McGrew, Jeffrey T.  
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
; FILE REFERENCE: 03260.0028  
; CURRENT APPLICATION NUMBER: US/09/904,536  
; CURRENT FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100  
; PRIOR FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-904-536-18

Query Match 89.7%; Score 1114; DB 10; Length 209;  
Best Local Similarity 100.0%; Pred. No. 4.1e-92;  
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPVYASNIQDEELCGGLMRVLVLAQRMM 86  
DB 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPVYASNIQDEELCGGLMRVLVLAQRMM 60  
QY 87 KTVAGSKQGLLEVRNTEIHFTVKCAFQPPSCLRFVQTNISRLQETSSEQVVALKFWIT 146  
DB 61 KTVAGSKQGLLEVRNTEIHFTVKCAFQPPSCLRFVQTNISRLQETSSEQVVALKFWIT 120  
QY 147 RQNFSCLELQCGDSSSTLPPWSPRLEATAPAPOPPLLLLVGLLLAAACLIH 206  
DB 121 RQNFSCLELQCGDSSSTLPPWSPRLEATAPAPOPPLLLLVGLLLAAACLIH 180  
QY 207 WQTRRRTPRPGEOVPPVPSPODLLVEH 235  
DB 181 WQTRRRTPRPGEOVPPVPSPODLLVEH 209

RESULT 7  
US-09-904-536-9  
; Sequence 9, Application US/09904536  
; Patent No. US20020111475A1  
; GENERAL INFORMATION:  
; APPLICANT: Gradidis, Thomas J.  
; APPLICANT: McGrew, Jeffrey T.  
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
; FILE REFERENCE: 03260.0028  
; CURRENT APPLICATION NUMBER: US/09/904,536  
; CURRENT FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100  
; PRIOR FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-904-536-9

```
Query Match      89.4%; Score 1110; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 9.3e-92;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 27 TODCSFQHSPISSDPAVKIRELSDYLLQDYPVTVASNIODEELCGGLMRLVLAQRMERL 86
    |||
    1 TODCSFQHSPISSDPAVKIRELSDYLLQDYPVTVASNIODEELCGGLMRLVLAQRMERL 60
DB

OY 87 KTVAGSKMOGLLEERVNTEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 146
    |||
    61 KTVAGSKMOGLLEERVNTEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 120
DB

OY 147 RQNFSCLELQCCQDSSSTLPWPMSRPLEATAPAPQPLLILLPVGILLAAACMLH 206
    |||
    121 RQNFSCLELQCCQDSSSTLPWPMSRPLEATAPAPQPLLILLPVGILLAAACMLH 180
DB

OY 207 WQTRRRTPRPGEOVPPVPSPODLLLVEH 235
    |||
    181 WQTRRRTPRPGEOVPPVPSPODLLLVEH 209
DB

RESULT 8
US-09-904-536-12
; Sequence 12, Application US/09904536
; Patent No. US2002011475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-12

Query Match      89.4%; Score 1110; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 9.3e-92;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 27 TODCSFQHSPISSDPAVKIRELSDYLLQDYPVTVASNIODEELCGGLMRLVLAQRMERL 86
    |||
    1 TODCSFQHSPISSDPAVKIRELSDYLLQDYPVTVASNIODEELCGGLMRLVLAQRMERL 60
DB

OY 87 KTVAGSKMOGLLEERVNTEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 146
    |||
    61 KTVAGSKMOGLLEERVNTEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 120
DB

OY 147 RQNFSCLELQCCQDSSSTLPWPMSRPLEATAPAPQPLLILLPVGILLAAACMLH 206
    |||
    121 RQNFSCLELQCCQDSSSTLPWPMSRPLEATAPAPQPLLILLPVGILLAAACMLH 180
DB

OY 207 WQTRRRTPRPGEOVPPVPSPODLLLVEH 235
    |||
    181 WQTRRRTPRPGEOVPPVPSPODLLLVEH 209
DB

RESULT 9
US-09-904-536-14
; Sequence 14, Application US/09904536
; Patent No. US2002011475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
```

```
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-14

Query Match      89.4%; Score 1110; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 9.3e-92;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 27 TODCSFQHSPISSDPAVKIRELSDYLLQDYPVTVASNIODEELCGGLMRLVLAQRMERL 86
    |||
    1 TODCSFQHSPISSDPAVKIRELSDYLLQDYPVTVASNIODEELCGGLMRLVLAQRMERL 60
DB

OY 87 KTVAGSKMOGLLEERVNTEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 146
    |||
    61 KTVAGSKMOGLLEERVNTEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 120
DB

OY 147 RQNFSCLELQCCQDSSSTLPWPMSRPLEATAPAPQPLLILLPVGILLAAACMLH 206
    |||
    121 RQNFSCLELQCCQDSSSTLPWPMSRPLEATAPAPQPLLILLPVGILLAAACMLH 180
DB

OY 207 WQTRRRTPRPGEOVPPVPSPODLLLVEH 235
    |||
    181 WQTRRRTPRPGEOVPPVPSPODLLLVEH 209
DB

RESULT 10
US-09-904-536-17
; Sequence 17, Application US/09904536
; Patent No. US2002011475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-17

Query Match      89.4%; Score 1110; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 9.3e-92;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 27 TODCSFQHSPISSDPAVKIRELSDYLLQDYPVTVASNIODEELCGGLMRLVLAQRMERL 86
    |||
    1 TODCSFQHSPISSDPAVKIRELSDYLLQDYPVTVASNIODEELCGGLMRLVLAQRMERL 60
DB

OY 87 KTVAGSKMOGLLEERVNTEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 146
    |||
    61 KTVAGSKMOGLLEERVNTEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 120
DB

OY 147 RQNFSCLELQCCQDSSSTLPWPMSRPLEATAPAPQPLLILLPVGILLAAACMLH 206
    |||
    121 RQNFSCLELQCCQDSSSTLPWPMSRPLEATAPAPQPLLILLPVGILLAAACMLH 180
DB

OY 207 WQTRRRTPRPGEOVPPVPSPODLLLVEH 235
    |||
    181 WQTRRRTPRPGEOVPPVPSPODLLLVEH 209
DB
```



